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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 15, 2004, 21:34:28; Search time 18 Seconds (without alignments) 1758.167 Million cell updates/sec Run on:

US-10-081-775-2 1718 1 MSSTLGHNYMESPHHTDVDPS......RKRVVRVFQSGQGMGIKASE 329 BLOSUM62 Gapop 10.0 , Gapext 0.5 Perfect score: Sequence: Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

olfactory receptor
odorant receptor
olfactory receptor olfactory receptor olfactory receptor odorant receptor lactory receptor olfactory receptor olfactory receptor olfactory receptor chemoreceptor TB33 hypothetical prote odorant receptor 2 odorant receptor 8 olfactory receptor olfactory receptor Description SUMMARIES 123701 E23701 JC5200 S51356 H45774 \$29708 JC4658 H23701 \$20573 \$29709 E45774 B23701 S29707 C23701 JC5836 S20571 F45774 S20572 A46247 A46750 JC5624 A57069 S29711 F23701 Query Match Length DB Score 433 4222 419 414.5 414.5 414.6 414.6 414.6 404.6 404.5 395.5 395.5 395.5 394.5 394.5 Result No.

RESULT 2

G45774

G45774

Gorant receptor 202 - channel catfish
C;Species: Ictalurus punctatus (channel catfish)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 04-Sep-1998
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 04-Sep-1998
R;Ngai, J; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.
Cell 72, 657-666, 1993
A;Title: The family of genes encoding odorant receptors in the channel catfish.
A;Reference number: A45774; MUID:93201590; PMID:7916654

| probable olfactory | Chemoreceptor 7864 | odorant recentor 3 | olfactory recentor | probable olfactory | odorant recentor 3 | olfactory recentor | odorant recentor 3 | odorant recentor 3 | olfactory recentor | odorant receptor (| chemorecentor TR56 | odorant recentor (| G protein-compled | G protein-confec | olfactory receptor |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|------------------|--------------------|
| A48413 | JC5202 | A45774 | 829710 | 358066 | C45774 | A23701 | B45774 | D45774 | D23701 | D40745 | JC5201 | B40745 | 829000 | 828998 | PC4369 |
| 7 | ~ | 7 | N | 7 | 7 | 7 | ~ | 7 | ~ | ~ | ~ | N | 7 | ~ | 7 |
| 312 | 318 | 328 | 307 | 160 | 328 | 333 | 328 | 328 | 317 | 222 | 315 | 222 | 234 | 234 | 264 |
| 21.9 | 21.9 | 21.7 | 21.6 | 21.4 | 21.4 | 21.4 | 21.3 | 20.8 | 20.5 | 19.8 | 18.9 | 17.9 | 17.4 | 17.4 | 17.4 |
| •• | | | | | | _ | 10 | Ŋ | ٣ | Н | 2 | 7 | σ | σ | σ |
| 376.5 | 376 | 372.5 | 371 | 368.5 | 367.5 | 367 | 366.5 | 356.5 | 353 | 34 | 325 | 30 | 299 | 299 | 299 |

ALIGNMENTS

| RESULT 1 AGOSTAL 1 AGOSTAL 1 AGOSTAL 1 AGOSTAL 1 AGOSTAL 2 AGOSTAL 2 AGOSTAL 2 AGOSTAL 2 AGOSTAL 3 A |
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Matches 107; Conservative
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                                                                                                                                                                          olfactory receptor F5
                                                                                   MK 306
                                                FQ 318
                                                317
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C.Species: Ictalurus punctatus (channel catfish)
C.Species: Ictalurus punctatus (channel catfish)
C.Accession: E45774
R;Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.
Cell 72, 657-666, 1993
A;Title: The family of genes encoding odorant receptors in the channel catfish.
A;Reference number: A45774; MUID:93201590; PMID:7916654
A;Reference number: A45774
A;Reference number: A6774
A;Reference number: A6774
A;Reference number: A6774
A;Reference number: A6774
A;Residues: 1-313 <NGA>
A;Nolecule type: mRNA
A;Residues: 1-313 <NGA>
C;Superimental source: olfactory epithelium
A;Note: sequence extracted from NCBI backbone (NCBIP:127748)
C;Superfamily: olfactory receptor OR14
C;Keywords: olfaction; transmembrane protein
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                                                                                                                                                                                                                                                                                   140
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                                                                                                                                                                                                                                                                                   LAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAMAFDRYVAICHPL
                                                                                                                                                                                                             22 FFLIGIPGL-EQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLCMLSTID
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not compared with conceptual translation
                                                                                                                                                                            Indels
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                                                                      (NCBIP:127746)
                                                                                                                                       Query Match 28.5%; Score 489.5; DB 2; Best Local Similarity 34.6%; Pred. No. 6e-36; Matches 102; Conservative 60; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127;
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Best Local Similarity 33.4%; Pred. No. 9.5e-34;
Matches 101; Conservative 65; Mismatches 127
A;Status: preliminary; not compared with conce.
A;Molecule type: mRNA
A;Residues: 1-328 «NGA»
A;Experimental source: olfactory epithelium
A;Note: sequence extracted from NBID backbone
C;Superfamily: olfactory receptor OR14
C;Keywords: olfaction; transmembrane protein
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olfactory receptor 114 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C;Accession: 123701
R;Buck, L; Axel, R.
R;Buck, L; Axel, R.
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for oc
A;Reference number: A23701; MUID:91191556; PMID:1840504
                                                                                                                                                                                                                                                                                               C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998
C;Accession: B23701
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for A;Title: A novel mulber: A23701; MUID:91191556; PMID:1840504
A;Accession: B23701
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 GTCGSHVCVILISYTPALFSFF----THRFGHHVPVHIHILLANVYLLLPPALNPVVYGV 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 MESPHHTDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKP
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A,Status: nucleic acid sequence not shown
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1-312 <BUC>
A,Cross-references: GB:M64391; NID:g205843; PIDN:AAA41754.1; PID:g205844
C,Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 313;
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ches 135;
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A;Residues: 1-313 <BUC>
A;Cross-references: GB:M64377
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 446; DB
; Pred. No. 4.2e
63; Mismatches
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33.3%;
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and male reproductive tissues.

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A;Cross-references: GB:U50947; NID:g1256388; PIDN:AAC52909.1; PID:g1256389
A;Accession: PC4302
                  Rithomas, M.B.; Haines, S.L.; Akeson, R.A.
Gene 178, 1-5, 1996
A.Title: Chemoreceptors expressed in taste, olfactory an
A;Reference number: JC5200; MUID:97080538; PMID:8921883
A;Accession: JC5200
A;Status: nucleic acid sequence not shown
       Accession: JC5200; PC4302
                                                                                                                                              A; Residues: 1-311 <THO1>
                                                                                                                             A, Molecule type: DNA
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                                                                                                                                                                                                            142 YATILTDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKLACGD 201
                                                                                                                                                                                                                                  202 TRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVIRLSSHEARSKALGTCGSHVCVILIS 261
                                                                                                                                                                                                                                                                                                   192 IYVNELMIYILGGLIIIIPFLLIVMSYVRIFFSILKFPSIQDIYKVFSTCGSHLSVVTLF 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olfactory receptor I3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Accession: E23701
R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular A;Reference number: A23701; MUD:91191556; PMID:1840504
                                                                   22 FFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHXPVYLFLCMLSTIDL
                                                                                           | |||:|
12 Filiglpipseyhilfyalflamyltiilgnilijuuvridshihmpmylflsnisesdi
                                                                                                                                      82 AASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAMAFDRYVAICHPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 LAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAMAFDRYVAICHPL
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                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                   YTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVVRV 316
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Cross-references: GB:M64385; NID:g205831; PIDN:AAA41748.1; PID:g205832 C;Superfamily: olfactory receptor OR14 C;Reywords: G protein-coupled receptor; transmembrane protein
                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
; Score 445; DB 2; Length 312;
; Pred. No. 5.1e-32;
58; Mismatches 133; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.3%; Score 434; DB 2; Length 310
33.8%; Pred. No. 4.8e-31;
ive 68; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: E23701
A;Status: nucleic acid sequence not shown
 25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 33.04
Matches 101; Conservative
Query Match 25.9
Best Local Similarity 34.6
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                    262
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A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: protein
A;Status: protein
A;Residues: 146-135,265-272 < THO2>
A;Experimental source: taste bud
C;Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction
C;Genetics:
G;Genetics:
C;Genetics:
C;Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S51356; 847014
R;Gat, U; Nekrasova, E: Lancet, D.; Natochin, M.
Bur. J. Biochem. 225, 1157-1168, 1998
A;Title: Olfactory receptor proteins. Expression, characterization and part:
A;Reference number: S51356; MUID:95045546; PMID:7957207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 IDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAMAFDRYVAICH
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34.9%; Pred. No. 5.9e-31;
iive 52; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 34.9
Matches 107; Conservative
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296 KGALKRL 302
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chemoreceptor TB334 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-Aug-1999

C.; Breer

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A,Molecule type: mRNA
A,Residues: 1-314 <RAM>
Fbuck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A,Reference number: A23701; MUID:91191556; PMID:1840504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: B37286
A;Status: mucleic acid sequence not shown; not compared with conceptual translation
A;Katus: mucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 193-236 <BUC>
A;Cross-references: B9:M64375; NID:g205811; PIDN:AAA41738.1; PID:g205812
C;Superfamily: olfactory receptor OR14
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
C;Accession: $29707; B37286
R;Raming, K; Krieger, J; Strotmann, J; Boekhoff, I.; Kubick, S.; Baumstark, Nature 361, 353-356, 1993
A;Title: Cloning and expression of odorant receptors.
A;Reference number: $29707; MUID:93149273; PMID:7678922
A;Accession: $29707
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                             SHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSS 240
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 SQFLLGLPIPPEHQHVFYAL-FLSMYLTTILGNLIIILLLLDSHLHTPMYLFLSNLSF
                                                                   20 SVFFLLGIP-GLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLCMLST
                                                                                                                                               HEARSKALGTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPV
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                                                                                                                                                                                                                                                                                           301 IYTLKTEEVMQAIKLLYK 318
                                                                                                                                                                                                                                                           301 VYGVKTKQIRKRVVRVFQ 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                           olfactory receptor OR5 - rat
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Best Local Similarity
Matches 97; Conserval
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                                     pug
submitted to the EMBL Data Library, July 1994
A,Description: Olfactory receptor proteins: expression, characterization and partial
A,Reference number: $47014
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C.Species: Ictalurus punctatus (channel catfish)

C.Species: Ictalurus punctatus (channel catfish)

C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 04-Sep-1998

C.Accession: H45774

R.Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.

Cell 72, 657-666, 1993

A.Title: The family of genes encoding odorant receptors in the channel catfish. A.Reference number: A45774; MUID:93201590; PMID:7916654

A.Accession: H45774

A.Accession: H45774

A.Accession: H5574

A.Residues: 1321 <NGA>

A.Residues: 1321 <NGA>

A.Residues: 1321 <NGA>

A.Residues: Offactory epithelium

A.Note: sequence extracted from NCBI backbone (NCBIP:127745)

C.Superfamily: olfactory receptor OR14

C.Keywords: olfaction; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 IAQAVLRLSSHEARSKALGTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANV- 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LHKPVYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTV 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 LLHTPMYYFLSSLSFVDLCYSTVITPKMLVNFLGKKONFITYSECMAQFFFFAIFVVTEGY 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 IFCSILRIRSSEGRSKAFGTCSSHLMAVGIFFGSITFMYLKPSSSNSLEQE---KVSSVF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                           54
                                                                                                                                                                                                                                                                                                                                                                                                       9 MESPHHTDVDPSVFFLLGIPG----LEQFHLWLSLPVCGLGTATIVGNITILVVVATEP
                                                                                                                                                                                                                                                                                                                                                                                                                                       VLHKPVYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNFCQSHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLVIG-----VDLFCIGLSYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 NMESPHHTDVDPSVFFLLG---IPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-309 <GAL>
A;Cross-references: EMBL:X80671; NID:G517365; PIDN:CAA56697.1; PID:G517366
C;Superfamily: olfactory receptor OR14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.4%; Score 419; DB 2; Length 321; ilarity 30.5%; Pred. No. 1.1e-29; Conservative 73; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                        Length 309;
                                                                                                                                                                                                                                                                                     Query Match 24.6%; Score 422; DB 1; Lu
Best Local Similarity 32.2%; Pred. No. 5.6e-30;
Matches 105; Conservative 65; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 YLLLPPALNPVVYGVKTKQIRKRVVR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : | | | | | : : | : : | : | XTTVIPMLNPLIYSLRNKDVKKALGR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 97; Conserv
                                                                                                A;Accession: S47014
A;Status: preliminary
                                                                                             Accession: S47014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65
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Olfactory receptor - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 18-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
C;Accession: JC4658
R;Crowe, M.L; Perry, B.N.; Connerton, I.F.
Gene 169, 247-249, 1996
A;Title: Olfactory receptor-encoding genes and pseudogenes are expressed in humans.
A;Reference number: JC4658; MUID:96194811; PMID:8647456
A;Reference number: JC4658; MUID:96194811; PMID:8647456
A;Receile type: DNA
A;Residues: 1-315 <CRO>
A;Cross-references: EMBL:X80391; NID:9516319; PIDN:CAA56602.1; PID:9516320
A;Residues: 1-315 <CRO>
A;Cross-references: EMBL:X80391; NID:9516319; PIDN:CAA56602.1; PID:9516320
A;Reperimental source: Olfactory epithelial cells
C;Comment: This receptor belongs to a family of ligand-binding proteins involved in sign.
C;Genetics:
A;Gene: Twbt
A;Map position: 17
C;Superfamily: olfactory receptor OR14
C;Superfamily: olfactory receptor OR14
C;Superfamily: olfactory receptor predicted <TMI>
F;60-81/Domain: transmembrane #status predicted <TM3>
F;01-123/Domain: transmembrane #status predicted <TM3>
F;101-123/Domain: transmembrane #status predicted <TM3>
F;139-220/Domain: transmembrane #status predicted <TM5>
F;239-262/Domain: transmembrane #st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTCGSHVC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 VILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVVRV 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |: | | :| : : : : : : | | valfygsgifnym--rlgstklsdkdygifnyvinpmlnpilysfrnpdvqsaiwrm 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
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olfactory receptor 19 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C;Accession: H23701
                                                                                                                                                                                                                      GTVIGLYLCPSANNSTVKETVMAMMITVVTPMLNPFIYSLRNRD
            CGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTCGSHVCVI
                                                         189 CSDTXINELMIPILGGLLIVIPFLLIVMTYVQIVCSILKVPSTRAIYKIFSTCGSHLSTV
                                                                                                                                                                        259 LISYTPALFSFFTHRFGHHVPVHI------HILLANVYLLLPPALNPVVYGVKTKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILLGLLEAPGLOPVVFVLFLFAYL-----VTVRGNLSILAAVLVEPKLHTPMYFFLGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STIDLAASVSTVPKLIAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAMAFDRYVAI
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                                                                                                                                                                                                                                                                                                                                     309 IRKRVVRV 316
                                                                                                                                                                                                                                                                                                                                                                                                           297 IKEALVRV 304
                                                                                                                                                                                                                                                       249 SLFY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
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C;Accession: C23701

R;Buck, L.; Axel, R.

Gell 65, 175-187, 1991

A;Title: A novel multigene family may encode odorant receptors: a molecular basis for chittle: A novel multigene family may encode odorant receptors: a molecular basis for chitchen carried acid sequence number: A23701

A;Rotatus: nucleic acid sequence not shown

A;Rotatus: nucleic acid sequence not shown

A;Rotatus: 1-311 < BUC>

A;Rotatus: nucleic acid sequence not shown

A;Rotatus: 1-311 < BUC>

A;Rotatus: nucleic acid sequence not shown

A;Rotatus: nucleic acid sequence nucle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 AHRCLQTPMYFFLCNLSFLEIWFTTACVPKTLATFAPRGGVISLAGCATQMYFVFSLGCT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.; Baumstark,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLRYATILITDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKLA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESTVLLAMAFDRYVAICHPLRYATILTDTIIAHIGVAAVVRG-SLLMLPCPFFIGRLNFC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
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C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Dacession: S29708
R;Raming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstar Nature 361, 353-356, 1993
A;Title 10 in 353-356, 1993
A;Feference number: S29707; MUID:93149273; PMID:7678922
A;Accession: S29708
A;Rodecule type: mRNA
A;Rodecule type: mRNA
A;Rodecule type: mRNA
C;Superfamily: olfactory receptor OR14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 SQFLLIGLPIPPEHWHLFYTL-LLAMYLTTILGNLIIIILILLDSNLHIPMYLFLSNLSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLVI----GVDLFCIGLSYALIAQAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRLSSHEARSKALGTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIH------ILLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 311;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.1%; Score 414.5; DB 2; Length 3: 31.4%; Pred. No. 2.6e-29; rative 59; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.1%; Score 414; DB 2; Length 312 32.1%; Pred. No. 2.9e-29; ive 64; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :: | || | :| :: | ::: | NT--IVTPVLNPFIYTLRNKDVKEALRR 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVYLLLPPALNPVVYGVKTKQIRKRVVR 315
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Accession: S20573
R.Parmentier, M.; Libett, F.; Schurmans, S.; Schiffmann, S.; Lefort, A.; Eggerickx, D.;
Nature 355, 453-455, 1992
A.;Title: Expression of members of the putative olfactory receptor gene family in mammali
A.Reference number: S20573
A.Reference number: S20573
A.Reference of the putative olfactory receptor gene family in mammali
A.Reference: EMBL: X64995; NID:92131132; PMID:1370859
A.Residues: 1-320 c.PAR.
A.Residues: 1-320 c.PAR.
A.Residues: 1-320 c.PAR.
A.Corser-references: EMBL: X64995; NID:932092; PIDN: CAA46128.1; PID:932093
C.Superfamily: olfactory receptor OR14
C.Reywords: G protein-coupled receptor; transmembrane protein
R;Buck, L.; Axel, R.

Cell 65, 175-187, 1991

A;Title: A novel multigene family may encode odorant receptors: a molecular basis for A;Title: A novel multigene family may encode odorant receptors: a molecular basis for A;Reference number: A23701; MUID:9119156; PMID:1840504

A;Reference number: A23701; MUID:9119156; PMID:1840504

A;Rocession: H23701

A;Rotatus: nucleic acid sequence not shown
A;Residues: 1-314 < BUC>
A;Residues: 1-314 < BUC>
A;Residues: 1-314 < BUC>
A;Residues: 1-314 < BUC>
C;Superfemily: olfactory receptor OR14
C;Reywords: G protein-coupled receptor; transmembrane protein
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                                                                                                                                                                                                                                                                                                  23.6%; Score 406; DB 2; Length 314;
29.7%; Pred. No. 1.5e-28;
Live 73; Mismatches 113; Indels 34; Gaps
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240 SVEGRKKAFATCASHLTVVIVHYSCASIAYLKPK-SENTREHDQ-LISVTYTVITFLLINP 297
121 TNCFLLTAMGYDRYVAICNPLRYMVIMNKRLRIQLVLGACSIGLIVAITQVTSVFRLPFC 180
                                                                                                                                         : : | : | : | : | : | : | : | : | : | 181 -ARKVPHFFCDIRPVMKLSCIDTTVNEIITLIISVLVUVVPMGLVFISYVLIISTIIKIA
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                                                                              180 QSHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLS
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298 VVYTLRNKEVKDALCR 313
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein September 15, 2004, 21:35:29; Search time 18 Seconds (without alignments) 943.608 Million cell updates/sec Run on:

US-10-081-775-2 1718 Perfect score:

1 MSSTLGHNWESPHHTDVDPS.....RKRVVRVFQSGQGMGIKASE 329 **BLOSUM62** Scoring table: Sequence:

389414 segs, 51625971 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgr2_6/ptcdata/2/iaa/5A COMB.pep:*
2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:* Issued Patents AA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | ж | | | SUMMARIES | |
|---------------|-------|----------------|-----------------------|----|-------------------|-------------------|
| Result No. | Score | Query Match | Query Match Length | DB | ID | Description |
| 7 | 861 | 50.1 | 320 | 4 | US-09-439-313-527 | Sequence 527, App |
| 7 | 861 | 50.1 | 320 | 4 | -215- | 527 |
| Э | 861 | 50.1 | 320 | 4 | -685-166A-5 | 527 |
| 4 | 856 | 49.8 | 320 | Н | US-08-465-980-2 | 2. Ar |
| 2 | 856 | 49.8 | 320 | N | US-09-053-303-2 | Seguence 2, Appli |
| 9 | 856 | 49.8 | 320 | 4 | 9-115- | , c |
| 7 | 856 | 49.8 | 320 | 'n | PCT-US95-07093-2 | ۲, |
| 89 | 429 | 25.0 | 321 | ٣ | US-08-748-506-18 | 18 |
| 6 | 428.5 | 24.9 | 321 | m | US-08-748-506-20 | 7 |
| 10 | 424 | 24.7 | 321 | m | US-08-748-506-10 | 10 |
| 11 | 423.5 | 24.7 | 321 | m | US-08-748-506-12 | 12, |
| 12 | 416.5 | 24.2 | 321 | m | US-08-748-506-11 | - |
| 13 | 413 | 24.0 | 284 | Н | US-08-118-270-61 | 61, |
| 14 | 413 | 24.0 | 284 | Ŋ | PCT-US93-08528-61 | 61, |
| 15 | 412.5 | 24.0 | 321 | m | US-08-748-506-19 | 19. |
| 16 | 410.5 | 23.9 | 321 | m | US-08-748-506-13 | 13, |
| 17 | 410 | 23.9 | 340 | 4 | US-09-546-986A-6 | 6 |
| 18 | 410 | 23.9 | 340 | 4 | US-09-524-730-6 | Sequence 6, Appli |
| 19 | 401 | 23.3 | 310 | 4 | US-09-546-986A-2 | 7 |
| 70 | 40 | 23.3 | 310 | 4 | US-09-524-730-2 | ď |
| 21 | 394.5 | 23.0 | 314 | m | US-08-988-876-7 | 7 |
| 22 | 393 | 22.9 | 296 | 0 | US-08-467-948A-2 | 7 |
| 23 | 393 | 22.9 | 296 | m | US-08-467-947A-2 | 7 |
| 24 | 388.5 | 22.6 | 309 | m | US-08-988-876-5 | 'n |
| 25 | 381 | 22.2 | 334 | 4 | -09-546-9 | Sequence 8, Appli |
| 56 | 381 | 22.2 | 334 | 4 | US-09-524-730-8 | 8 |
| 27 | 374 | 21.8 | 316 | ~ | US-08-827-291A-2 | 7 |

| Appli | Appli | Appli | Appli | Appli | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl |
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| Sequence | Sequence | Sequence | Sequence | Seguence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Seguence | Seguence | Seguence | Sequence | Seguence |
| US-08-988-876-6 | US-08-465-980-3 | US-09-053-303-3 | US-09-339-115-3 | PCT-US95-07093-3 | US-08-118-270-67 | PCT-US93-08528-67 | US-08-748-506-22 | US-08-748-506-23 | US-08-467-948A-27 | US-08-467-947A-27 | US-08-118-270-62 | PCT-US93-08528-62 | US-08-118-270-65 | PCT-US93-08528-65 | US-08-748-506-24 | US-08-118-270-68 | PCT-US93-08528-68 |
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| 333 | 247 | 247 | 247 | 247 | 284 | 284 | 327 | 327 | 222 | 222 | 277 | 277 | 286 | 286 | 327 | 277 | 277 |
| 21.4 | 21.0 | 21.0 | 21.0 | 21.0 | 20.3 | 20.3 | 19.9 | 19.9 | 19.8 | 19.8 | 19.8 | 19.8 | 19.4 | 19.4 | 19.3 | 19.2 | 19.2 |
| 367 | 361 | 361 | 361 | 361 | 349.5 | 349.5 | 341.5 | 341.5 | 341 | 341 | 340 | 340 | 333.5 | 333.5 | 332 | 330 | 330 |
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                                                                          | APPLICANT: Xu, Jiangchun | APPLICANT: Xu, Jiangchun | APPLICANT: Mitcham, Jennifer L. | APPLICANT: Head, Steven G. | APPLICANT: Reade, Steven G. | APPLICANT: Reade, Steven G. | APPLICANT: Retter, Mark | APPLICANT: Retter, Mark | APPLICANT: Solk, John | APPLICANT: Solk, John | APPLICANT: OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND | TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER | FILE REFERENCE: 210121.427C9 | CURRENT APPLICATION NUMBER: US/09/439,313 | CURRENT APPLICATION NUMBER: US/09/439,313 | SOFTWARE: FastSEQ for Windows Version 3.0 | SEQ ID NOS: 575 | TENNIOR: 2300
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53.8%; Pred. No. 8e-74;
tive 49; Mismatches 89; Indels
                   Sequence 527, Application US/09439313 Patent No. 6329505
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Best Local Similarity 53.8%
Matches 161; Conservative
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CORGANISM: Homo sapiens
US-09-439-313-527
US-09-439-313-527
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249 AFYVPLIGLSVVHRFGNSLHPIVRVVMGDIYLLEPDVINPLIYGAKTKQIRTRVLAMFK 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210.1.42717C17

CURRENT APPLICATION NUMBER: US/09/636,215

CURRENT FILING DATE: 2000-08-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 527, Application US/09685166A Patent No. 6630305 GENERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Micham, Janifer L. APPLICANT: Hicham, Janifer L. APPLICANT: Harlocker, Susan L.
                                                            Jaywence 527, Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: YOUR
                                                                                                                                                             Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Hepler, William
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Wang, Aijun
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US-09-685-166A-527
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APPLICANT:
APPLICANT:
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APPLICANT:
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140 LRYATILTDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKLAC 199
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT APPLICATION NUMBER: US/09/685,166A
SURRENT SELING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 320,
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Patent No. 5756309

GENERAL INFORMATION:

APPLICANT: Li, Yi

APPLICANT: Rosen, Craig A.

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70

YUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.1%; Score 861; DB 4, 53.8%; Pred. No. 8e-74;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
                                                                                                                               Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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                                                                            Fanger, Gary R.
Retter, Marc W.
                                                                                                                                                                                                                                                                          Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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STREET: 6 Becker
CITY: Roseland
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PRIOR APPLICATION DATA:
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ZIP: 0706
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                                                                                                                                                                                                                                                                                                                                                               ; DB 1; Length 320;
2.4e-73;
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STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
CORRESPONDENCE ADDRESS:
OPERATING SYSTEM: PC-DOS/WS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,980
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGRAT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEFONDE: 201-994-1700
TELEFAK: 201-994-1700
TELEFAK: 201-994-1700
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                             ; Score 856; DB
; Pred. No. 2.4e-
48; Mismatches
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Patent No. 5948890
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               49.8%;
54.2%;
                                                                                                                                                                                                                                                         LENGTH: 320 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                           Matches 160; Conservative
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                            linear
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Best Local Similarity
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84 SVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAMAFDRYVAICHPLRYA 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 PALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVVRVFQ 318
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GENERAL INFORMATION:

APPLICANT: Bi, Yi

APPLICANT: Bosen, Craig A.

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70

NUMBER OF SEQUENCES: 8

NUMBER OF SEQUENCES: 8

NUMBER OF SEQUENCES: 8

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN, CECCHI, STREET: 6 BECKET FARM Road

CITY: Roseland

CITY: New Jersey
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                49.8%; Score 856; DB 2;
54.2%; Pred. No. 2.4e-73;
tive 48; Mismatches 87
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELECHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6372891
                                                                                                                                                                                                                  TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 320 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.24
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-053-303-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 PALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVVRVFQ 318
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54.2%; Pred. No. 2.4e-73;
ive 48; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Roben, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLGTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07093
                                                                                  325800-446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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 09/053,303
                           ATTORNEY AGENT

NAME: Ferraro, Gregory D.

REGISTRATION UNDRER: 36,136

REFERENCE/DOCKET NUMBER: 3258

TELECOMMUNICATION INFORMATION:

TELEFROM 201-994-1700

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 Becker Farm Road
                                                                                                                                                  TYPE: amino acids
TOPOLOGY: limit
                                                                                                                                                                                                                                                                                               Best Local Similarity 54.2%
Matches 160; Conservative
                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6 Becarries Roseland STATE: New Jersey
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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204 PNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTCGSHVCVILISYT 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 TILTDTIIAHIGVAAVVRGSILMLPCPFFIGRINFCQSHVILHTYCEHMAVVKLACGDTR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 LLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLCMLSTIDLAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 PLIGLSVVHRFGNSLHPIVRVVMGDIYLLLPPVINPIIYGAKTKQIRTRVLAMFK 307
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49.8%; Score 856; DB 5; Length 320;
Best Local Similarity 54.2%; Pred. No. 2.4e-73;
Matches 160; Conservative 48; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPANIOS SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 7494
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
NAME: FEITATO, Gregory D.
REGIGSTRATION NUMBER: 36,134
REFRENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312-616-5700 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein PCT-US95-07093-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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ZIP: 60601-6780
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US-08-748-506-18
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us-10-081-775-2.rai

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48 IIVGNITILVVVATEPVLHKPVYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASAC 107
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-748-506-10
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                   Query Match
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Matches 9
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                                                                                                                                                                                                                                                                                                                                                                               104 ATQMFFFAFFGITECCLLAAMAFDRCMAICSPLHYATRMSREVCAHLAIVSWGMGCIVSL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 PCPFFIGRINFCOSHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 LAHMFFIHAFCMMESTVLLAMAFDRYVAICHPLRYATILTDTIIAHIGVAAVVRGSLLML 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 GQINFIPSINFCGPCEIDHFFCDLPPLALACGDISQNEAAIFVVAVLCISSPFLLIIYS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 YALIAQAVLRLSSHEARSKALGTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLA 287
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В
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STATE: LL
COUNTRY: US
COUNTRY: US
ZIP: 60601-6780

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPOTAR: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FPILING DATE: 08-NOV-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
FREFRENCE/DOCKET NUMBER: 74940
TELECHOMUNICATION INFORMATION:
TELECHOMUNICATION NIPORMATION:
TELECHOMUNICATION NIPORMATI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
CITY: Chicago
                                : 321 amino acids
amino acid
                                                                                                                                                                                                            Query Match
Best Local Similarity 34.8 Matches 97; Conservative
SEQUENCE CHARACTERISTICS
                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: protein
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US-08-748-506-20
                             LENGTH:
                                                             TYPE:
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87 TVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAMAFDRYVAICHPLRYATIL 146
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                                                                                                                                                                                                                                                                                                                                                                             203 AAIFVAAVLCIFSPFLLIISSYVRILVAVLVMPSPEGRHKALSTCSSHLLVVTLFYGSTS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                   267 FSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVVRVFQSGQGMGIK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                       26 VPG-ECFLEFILILMFL--VSLTGNILIALAICTSPSLHTPMYFFLANLSLIEIGYTCS 82
                                                                                   27 IPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLCMLSTIDLAASVS
                                                                                                                                                                                                                                                            147 IDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKLACGDTRPNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Gaps
                                                   11;
         Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.7%; Score 424; DB 3; Length 321; 34.4%; Pred. No. 2e-32; ive 48; Mismatches 127; Indels
                                                 Indels
24.9%; Score 428.5; DB 3; 35.3%; Pred. No. 7.6e-33; ive 51; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES:
ADDRESSPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-109-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08748506
Patent No. 6159707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                      Best Local Similarity 35.3%
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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147 IDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKLACGDTRPNR 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 AAIFVAAILCISSPFLVILYSYVRILVAVLVMPSPEGRHKALSTCSSHLLVVTLFYGSVS 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 VIPKMIQSLVSBARBİSRBGCATQMFFFTFFGITECCLLAAMAFDRCMGİCSPLHYATRM 142
SRGVCAYLAIVSWVWGCIVGLGQTNFIFSLNFCGPCEIDHFFCDLPFLLALACGDTSQNE 202
                                                                                         207 VYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTCGSHVCVILISYTPAL 266
                                                                                                                                  AAIFVAAVLCIFSPPLLIISSYVRILVAVLVMPSPEGRHKALSTGSSHLVVTLFYGSTS 262
                                                                                                                                                                                                                  267 FSFFTHREGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVVRVFQSGQGMGIK 326
                                                                                                                                                                                                                                                     27 IPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLCMLSTIDLAASVS
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; Pred. No. 1e-31;
48; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-08-748-506-11
i Sequence 11, Application US/08748506
j Patent No. 6159707
i GENERAL INFORMATION:
i APPLICANT: Ronnett et al.
i TITLE OF INVENTION: NOVEL SPERM RECEPTORS
i NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
i ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74
TELECOMOUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFEAX: 312-616-5700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 24.2%;
Best Local Similarity 34.1%;
Matches 102; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                         143
                                                                                                                                                                                                                                                                                         263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 IDTIIAHIGVAAVVRGSLIMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKLACGDTRPNR 206
                                                                                                                                                                                                                                         164 GQTNPIFSLNFCGPCEIDHFFCDLPPLLALACGDTSQNEAAIFVVAVLCISSPFLLIIXS 223
                                                                                                                                                                                                                                                                                                                            228 YALIAQAVLRISSHEARSKALGTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLA 287
                                                                                                                                                                                                                                                                                                                                                                     224 YVKILIAVLLMPSPEGRHKALSTCSSHLLVVTLFYGSACITYLRPKSSH--SPGMDKFLA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 IPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLCMLSTIDLAASVS 86
               SLIGNILIVLAICTSPSLHIPMYFFLANLSLLEIGYICSVIPKMLQSLVSEAREISREGC 103
                                                                               108 LAHMFFIHAFCMMESTVLLAMAFDRYVAICHPLRYATILTDTIIAHIGVAAVVRGSLLML 167
                                                                                                                                  104 ATQMFFFAFFGITECCLLAAMAFDRCMAICSPLHYATRMSREVCAHLAIVSWGMGCIVSL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 vPG-ECFLLFTLILLMFL--VSLTGNTLIALAICTSPSLHTPMYFFLANLSLLBIGYTCS
                                                                                                                                                                                                      168 PCPFFIGRLNFCQSHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY:
STATE: IL
COUNTRY: US
ZUP: 60601-6780
ZIP: 60601-6780
COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLANCE FORM:
SOFTWARE: PETENT DE-DOS/MS-DOS
SOFTWARE: PETENT DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
FILEPHONE: 312-616-5600
TELEPHONE: 312-616-5600
TELEPHONE: 312-616-5600
TELEPHONE: "TELEPHONE: "T
                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 NVYLLLPPALNPVVYGVKTKOIRKRVVRVFQSGQGMGIK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 423.5; DB 3;
Pred. No. 2.3e-32;
1; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Romett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08748506
Patent No. 6159707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.7%; Scoilarity 35.0%; Pre
Conservative 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two P. CITY: Chicago
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167 LPCPFFIGRLNFCQSHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGL 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 CLAHMFFIHAFCMMESTVLLAMAFDRYVAICHPLRYATILTDTIIAHIGVAAVVRGSLLM 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 CLTQLYFLAVFGNMDNFLLAVMSYDRÝVAICHPLHÝTTÍRQLCVLLVVGSWVANMNCLL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 SYALIAQAVLRLSSHEARSKALGTCGSHVCVILISYTPALFSFF----THRFGHHVPVHI
                                                                                                     Sequence 61, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.0%; Score 413; DB 5; Length 284; 33.6%; Pred. No. 1.9e-31;
----AVMYAVVTPMINPFIYSLRNSDMKAALRKVLAMRFPSKQ 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 HILLANVYLLLPPALNPVVYGVKTKQ----IRKRVVRVFQSGQ 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 ----AVMYAVVTPMINPFIYSLRNSDMKAALRKVLAMRFPSKQ 284
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PLAN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56; Mismatches 114;
                                                                                                                                                                                                                                                    E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MURPHY=2 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Townsend, Kevin G. REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 amino acids
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS: ADDRESSE: BROWDY AN
                                                                                                                                                                                                                                                                                             Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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USA
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                                                                                                                                                                                                                                                                                                                                                         20004
                                                                                     PCT-US93-08528-61
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                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95;
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  246
                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                           RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 LPCPFFIGRLNFCQSHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGL 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYALIAQAVLRLSSHEARSKALGTCGSHVCVILISYTPALFSFF----THRFGHHVPVHI 282
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                                       47 ATIVGNITILVVVATEPVLHKPVYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 ATVLGNLLIILAIGGBSRIHTPMYFFLSNLSFVDVCFSSTTVPKVLANHILGSQAISFSG
                                                                                                                                                       Sequence 61, Application US/08118270

Patent No. 5508384

GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schueter, David I.
TITLE OF INVENTION: POLYEPPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.0%; Score 413; DB 1; Length 284; 33.6%; Pred. No. 1.9e-31; ative 56; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 HILLANVYLLLPPALNPVVYGVKTKQ----IRKRVVRVFQSGQ 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/ARTHORMATION:
NAME: TOWNSEND, Kevin G.
NAME: TOWNSEND, Kevin G.
REGISTRATION NUMBER: 34,033
REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MURPHY=2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 amino acids
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                RESULT 13
US-08-118-270-61
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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87 TVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAMAFDRYVAICHPLRYATIL 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 VPG-ECFLLFTLILIAMEL--VSLTGNALIALAACTSPSLHTPMYFFLANLSLLEIGYTCS 82
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Sequence 19, Application US/08748506

Patent No. 6159707

GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INTENTION:
CORRESPONDENCES: 31
CORRESPONDENCES: 12
CORRESPONDENCES: Leddig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Leddig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Leddig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STREET: Leddig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
COUNTRY: US
COUNTRY: US
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
PRIOR APPLICATION ON 435
CLASSIFICATION 1435
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 312-616-5600
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LEGGTH: 321 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: unknown
US-08-748-506-19
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September 15, 2004, 21:36:29 , Search time 50 Seconds (without alignments) 2110.138 Million cell updates/sec
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1718
1 MSSTLGHNMESPHHTDVDPS......RKRVVRVFQSGQGMGIKASE 329
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/ cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US06_PUBCCMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US08_PUBCCMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US08_PUBCCMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US08_PUBCCMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1335176 seqs, 320689617 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                Run on:
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| | | Description | Sequence 2. Appli | Seguence 261. App | Sequence 261. Ann | Seguence 354. App | • | Sequence 38. Appl | 798 | 924 | Sequence 19. Appl | Sequence 834. App | 316 | 946 | 158 | Semience 820 App | Sequence 45, Appl | |
|-----|--------|-----------------|-------------------|-------------------|-------------------|--------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|--|
| | | CI . | US-10-081-775-2 | US-09-886-055-261 | US-09-804-291-261 | US-10-343-650A-354 | US-10-025-806-36 | US-10-025-806-38 | US-10-292-798-798 | US-10-017-161-924 | US-10-297-021-19 | US-10-292-798-834 | US-10-343-650A-316 | US-10-017-161-946 | US-10-387-629-158 | US-10-292-798-820 | US-10-467-252-45 | |
| | | DB | 14 | σ | 10 | 12 | 14 | 14 | 15 | 14 | 16 | 15 | 12 | 14 | 15 | 15 | 16 | |
| | | Match Length DB | 329 | 329 | 329 | 329 | 329 | 329 | 329 | 321 | 321 | 299 | 329 | 329 | 329 | 329 | 329 | |
| مين | Query | Match | 100.0 | 98.4 | 98.4 | 98.4 | 98.4 | 98.4 | 98.4 | 96.0 | 96.0 | 54.5 | 54.2 | 54.2 | 54.2 | 54.2 | 54.2 | |
| | | Score | 1718 | 1691 | 1691 | 1691 | 1691 | 1691 | 1691 | 1649 | 1649 | 936.5 | 931.5 | 931.5 | 931.5 | 931.5 | 931.5 | |
| | Result | No. | ч | 7 | e | 4 | Ŋ | 9 | 7 | ထ | 6 | 10 | 11 | 12 | 13 | 14 | 15 | |

| Semience 2. Appli | Sequence 20. Appl | Sequence 113, App | Sequence 113. App | Seguence 214, App | Sequence 10. Appl | Sequence 16, Appl | 784 | 18 | Sequence 26, Appl | 878 | Sequence 101, App | Sequence 101, App | Sequence 56. Appl | Segmence 101. App | Seguence 198. App | Sequence 5. Appli | Sequence 55. Aprol | Sequence 38. Appl | Sequence 2. Appli | Sequence 4, Appli | Sequence 14, Appl | Sequence 54, Appl | Sequence 99, Appl | Sequence 76, Appl | | 36 | .09 | 14, | Sequence 14, Appl |
|--------------------|--------------------|-------------------|---------------------|----------------------|--------------------|--------------------|---------------------|--------------------|--------------------|---------------------|-------------------|---------------------|-------------------|-------------------|----------------------|-------------------|--------------------|-------------------|-------------------|-------------------|---------------------|-------------------|-------------------|-------------------|-------|-------|---------------------|--------|--------------------|
| 2 US-10-182-822A-2 | 4 US-10-044-643-20 | US-09-886-055-113 | 0 US-09-804-291-113 | 2 US-10-343-650A-214 | 4 US-10-220-382-10 | 4 US-10-044-643-16 | 5 US-10-292-798-784 | 4 US-10-044-643-18 | 4 US-10-025-806-26 | 4 US-10-017-161-878 | US-09-886-055-101 | 0 US-09-804-291-101 | | | 2 US-10-343-650A-198 | | 4 US-10-044-643-55 | | 4 US-10-025-806-2 | 4 US-10-025-806-4 | 0 US-09-966-459A-14 | | | | | | 5 US-10-005-041A-60 | | 5 US-10-466-720-14 |
| 326 1 | 311 1 | 311 9 | 311 1 | 311 1 | 311 1 | 311 1 | 311 1 | 311 1 | 329 1 | 314 1 | 318 9 | 318 1 | Н | Н | - | ٦ | ٦ | ٦ | H | 322 1 | 326 1 | Н | Н | 7 | Ч | - | Н | 326 10 | 321 10 |
| 53.6 | 52.8 | 52.6 | 52.6 | 52.6 | 52.6 | 52.6 | 52.6 | 52.6 | 52.5 | 51.8 | 51.8 | 51.8 | 51.8 | 51.8 | 51.8 | 51.8 | 51.8 | 51.8 | 51.8 | 51.7 | 51.7 | 51.7 | 51.7 | 51.7 | 51.7 | 51.7 | 51.7 | 51.7 | 51.6 |
| 920 | 907 | 904 | 904 | 904 | 904 | 904 | 904 | 903 | 901.5 | 889.5 | 889.5 | 889.5 | 889.5 | 889.5 | 889.5 | 889.5 | 889.5 | 889.5 | 889.5 | 888.5 | 887.5 | 887.5 | 887.5 | 887.5 | 887.5 | 887.5 | 887.5 | 887.5 | 886.5 |
| 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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Sequence 2, Application US/10081775
Publication No. US20030060409A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: RECEPTOR, HGPRBMY25, EXPRESSED HIGHLY IN IMMUNE-RELATED TISSUES
ITILE OF INVENTION: RECEPTOR, HGPRBMY25, EXPRESSED HIGHLY IN IMMUNE-RELATED TISSUES
ITILE REPERENCE: D0126 NP
CURRENT APPLICATION NUMBER: US 60/270,134
PRIOR APPLICATION NUMBER: US 60/270,134
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 60/270,134
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.0
SSEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 329; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: homo sapiens
US-10-081-775-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-081-775-2
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 261
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                       181 SHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSS 240
                                                                                            SHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSS 240
                                                                       HEARSKALGTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPV 300
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                                                                                                                                                                                                                                   RESULT 2
US-09-886-055-261
US-09-886-055-261
US-09-886-055-261

| Sequence 261, Application US/09886055
| Patent No. US20020132273A1
| GENERAL INFORMATION:
| APPLICANT STRYER, LUBERT
| APPLICANT ZOZULYA, SERGEY
| TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
| FILE REFERENCE: 078003-0277150
| CURRENT APPLICATION NUMBER: US/09/886,055
| CURRENT RILING DATE: 2001-06-22
| PRIOR APPLICATION NUMBER: 60/213,812
| PRIOR APPLICATION NUMBER: 60/213,812
| SOFTWARE: Patentin Ver. 2.1
| SEQUENCE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSSTLGHNMESPNHTDVDPSVFFLLGIPGLEQFHLMLSLPVGGLGTATIVGNITILVVVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSS
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Publication No. US20030088059A1
GENERAL INFORMATION:
A PAPLICANT: ZOZULA, SERGEY
ITILE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
FILE REPERENCE: P 0278005
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TYPE: PRT
CRGANISM: Homo sapiens
US-09-886-055-261
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APPLICANT: HAGA, TATSUTA
ITILE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
ITILE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: 31671-186347
CURRENT APPLICATION NUMBER: US/10/343,650A
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: JP 2000/237818
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 694
SOFTWARE: PALCHIN Ver. 2.1
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Best Local Similarity 98.8%; Pred. No. 9.5e-153;
Matches 325; Conservative 1; Mismatches 3;
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CURRENT APPLICATION NUMBER: US/09/804,2
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/188,914
PRIOR FILING DATE: 2000-03-13
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PRILING DATE: 2000-03-24
PRIOR PELLING DATE: 2000-03-24
PRIOR PELLING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-24
PRIOR FILING DATE: 2000-06-26
PRIOR PAPLICATION NUMBER: 60/139,849
PRIOR PELLING DATE: 2000-06-23
PRIOR PELLING DATE: 2000-06-36
PRIOR FILING DATE: 2000-08-16
PRIOR FILING DATE: 2000-08-16
PRIOR PELLING DATE: 2000-09-16
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US-10-025-806-36
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                                                                                                              Gaps
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APPLICANT: Malyankar, Uniel
APPLICANT: Abong, Haihong
APPLICANT: Ellerman, Karen
APPLICANT: Wolench, Adam
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-224 AB
CURRENT APPLICATION NUMBER: U6/25,806
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/256,635
PRIOR PILING DATE: 2000-12-18
PRIOR PPLICATION NUMBER: 60/259,743
PRIOR FILING DATE: 2001-01-04
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                                                                                   Length 329;
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                                                                                Score 1691; DB 12;
Pred. No. 9.5e-153;
1; Mismatches 3;
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APPLICANT: Li, Li
APPLICANT: Ballinger, Robert
APPLICANT: Kekuda, Ramesh
APPLICANT: Colman, Steven
APPLICANT: Colman, Steven
APPLICANT: Colman, Steven
APPLICANT: Colman, Steven
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Publication No. US20030198955A1
GENERAL INFORMATION:
                                                                                98.4%;
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Peyman, John
MacDougall, John
Stone, David
Vernet, Corine
Shenoy, Suresh
Gunther, Erik
Millet, Isabelle
TChernev, Velizar
Anderson, David
Gusev, Vladimir
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Edinger, Shlomit
Gerlach, Valerie
Sciore, Paul
                                                                           Query Match 98.4
Best Local Similarity 98.8
Matches 325, Conservative
              ; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-650A-354
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US-10-025-806-36
SEQ ID NO 354
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TEPVLHKPVYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMM 120
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PRIOR PILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-01-01-19
PRIOR PILING DATE: 2001-01-01-19
PRIOR APPLICATION NUMBER: 60/26,499
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-02-26
PRIOR PILING DATE: 2001-02-08
PRIOR PILING DATE: 2001-02-08
PRIOR PILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 60/275,946
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-04-23
PRIOR PILING DATE: 2001-04-16
PRIOR PILING DATE: 2001-04-16
PRIOR PILING DATE: 2001-04-16
PRIOR PILING DATE: 2000-12-1
PRIOR PILING DATE: 2000-12-1
PRIOR PILING DATE: 2000-12-1
PRIOR PILING DATE: 2001-04-16
PRIOR PILING DATE: 2001-04-16
PRIOR PILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
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; APPLICANT: Li, Li, APPLICANT: Li, Li, APPLICANT: Ballinger, Robert; APPLICANT: Rekuda, Ramesh; APPLICANT: Seytek, Kimberly; APPLICANT: Colman, Steven; APPLICANT: Colman, Stacie
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Best Local Similarity 98.8
Matches 325; Conservative
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WES-10-292-798-798

Sequence 798, Application US/10292798

Sequence 798, Application US/10292798

GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAL, KIYORIA
APPLICANT: ASAL, KIYORIA
APPLICANT: ABURATANI, HIROYUKI
ITILE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT FILING DATE: 2002-11-13
CURRENT FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR PLICATION NUMBER: 10 2001-246789
PRIOR PLICATION NUMBER: 3001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-292-798-798
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APPLICANT: Anderson, David
APPLICANT: Anderson, Uriel
APPLICANT: To Anderson, Uriel
APPLICANT: To Anderson, Wilden
APPLICANT: To Anderson, Malen
APPLICANT: To Anderson, Malen
APPLICANT: To Anderson, Malen
APPLICANT: Woldenc, Adam
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-224 AB
CURRENT FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-01-04
PRIOR PRILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR PRILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-22-08
PRIOR FILING DATE: 2001-01-22-08
PRIOR FILING DATE: 2001-02-24
PRIOR FILING DATE: 2001-03-24
PRIOR PRILING DATE: 2001-03-24
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-16
PRIOR PRILING DATE: 2001-04-16
PRIOR FILING DATE: 2001-04-18
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Edinger, Shlomit Gerlach, Valerie Sciore, Paul Smithson, Glennda Peyman, John MacDougall, John Stone, David Vernet, Corine Shenoy, Suresh Gunther, Erik Millet, Isabelle Tchernev, Velizar Anderson, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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APPLICANT: SUMA, MAKIKO
APPLICANT: AKIYAM, YUTAKA
APPLICANT: AKIYAM, YUTAKA
APPLICANT: ABURATAN, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENITON: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT ELING DATE: 2002-11-13
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SSOFITAND APPLICATION NUMBER: 12001-246789
NUMBER OF SEQ ID NOS: 2070
SSOFITAND APPLICATION NUMBER: 2001-6-18
NUMBER OF SEQ ID NOS: 2070
SSOFITAND APPLICATION NUMBER: 2001-6-18
NUMBER OF SEQ ID NOS: 2070
SSOFITAND APPLICATION NUMBER: 2001-6-18
NUMBER OF SEQ ID NOS: 2070
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                              ; FEATURE:
; NAME/KEY: misc feature
; CTHER INFORMATION: Incyte ID No. US20040023294A1 7476077CD1
US-10-297-021-19
                                                                                                                                                                                            Indels
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58.4%; Pred. No. 7.2e-81;
live 48; Mismatches 74; Indels
                                                                                                                                              Score 1649; DB 16;
Pred. No. 9.3e-149;
1; Mismatches 3;
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                                                                                                                                           Query Match
Best Local Similarity 98.8%;
Matches 317; Conservative
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Best Local Similarity 58.4;
Matches 173; Conservative
         ORGANISM: Homo sapiens
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US-10-292-798-834
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APPLICANT: THORNTON, Michael
APPLICANT: THORNTON, Michael
APPLICANT: U.V. Yan
APPLICANT: U.V. Yan
APPLICANT: U.V. Yan
APPLICANT: GANDHI, Ameena R.
APPLICANT: GANDHI, Ameena R.
APPLICANT: AU-YOUNG, Janice
TILLE OF INVENTION G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: SF-0781 PCT
CURRENT FILING DATE: 2001-05-22
PRIOR PELICATION NUMBER: 60/206,222; 60/207,476; 60/208,834; 60/208,861; 60/209,868
PRIOR FILING DATE: 2000-05-22; 2000-06-02; 2000-06-07
NUMBER OF SEQ ID NOS: 46
SOFTANCE: PERL PROGram
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                APPLICANT: ASAI, KIYOSHI
APPLICANT: AKITAMA, YUTAKA
APPLICANT: ARKITAMA, YUTAKA
APPLICANT: ABREATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
FRIOR APPLICATION NUMBER: US/10/017,161
FRIOR PILING DATE: 2002-12-18
FRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOSTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                    96.0%; Score 1649; DB 14;
98.8%; Pred. No. 9.3e-149;
tive 1; Mismatches 3;
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Publication No. US20040023294A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: INCTE GENOMICS, INC.
APPLICANT: PATTERSON, Chandra
APPLICANT: TRIBOULEY, Catherine M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YAO, Monique G.
GRIFFIN, Jennifer A.
THORNTON, Michael
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.8
Matches 317; Conservative
APPLICANT: SUWA, MAKIKO
                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           US-10-017-161-924
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LENGTH: 321
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APPLICANT:
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TYPE: PRT
ORGANISM: Homo Sapiens
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                                                                                                        ORGANISM: Homo
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                                                                                                                          US-10-017-161-946
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LENGTH: 329
                                                                       LENGTH: 329
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                                                                           78
NRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTCGSHVCVILISYTP 264
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                                                                                                                                             240 GLFSFYTQRFGQHVPRHIHILLADLYLVVPPMLNPIIYGMKTKQIMDGALRLLKWG 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 946, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: ARIXAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT FALICATION NUMBER: US/10/017,161
; CHRRENT FILIGO DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
                                                                                                                                                                                                               RESULT 11
US-10-343-650A-316

Sequence 316, Application US/10343650A

Publication No. US20040067499A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE REFERENCE: 31671-166347

CURRENT FILING DATE: 2003-07-21

PRIOR APPLICATION NUMBER: US/10/343,650A

CURRENT FILING DATE: 2003-07-21

PRIOR APPLICATION NUMBER: UP 2000/237818

PRIOR APPLICATION NUMBER: JP 2001/34434

PRIOR APPLICATION NUMBER: JP 2001/34434

PRIOR PILING DATE: 2001-02-13

NUMBER OF SEQ ID NOS: 694

SEQ ID NO 316

LENGTH: 329
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Best Local Similarity 59.9%
Matches 179; Conservative
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Sequence 158, Application US/10387629

Sequence 158, Daylication US/2030221205A1

Publication No. US20030221205A1

GENERAL INFORMATION:

APPLICANT: ChemCom S.A.

APPLICANT: Velichen, Alex

TITLE OF INVENTION: Olfactory and Pheromones G-Protein coupled Receptors

TITLE OF INVENTION: Olfactory and Pheromones G-Protein coupled Receptors

CURRENT APPLICATION NUMBER: US/10/387,629

CURRENT FILING DATE: 2003-03-13

NUMBER OF SEQ ID NOS: 254

SOFTWARE: Patentin version 3.1
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59.9%; Pred. No. 2.4e-80;
tive 42; Mismatches 77; Indels
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 946
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                                                                                                                                Sequence 820, Application US/10292798
| Publication No. US20030235833A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: SUMA, MAKIKO
| APPLICANT: AKIYAMA, YUTAKA
| APPLICANT: AKIYAMA, YUTAKA
| APPLICANT: ABURATANI, HIROYUKI
| TITLE OF INVENITON: GIANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
| FILE REFREENCE: 084335/166
| CURRENT APPLICATION NUMBER: US/10/292,798
| CURRENT FILING DATE: 2002-11-13
| PRIOR FILING DATE: 2001-12-18
| PRIOR FILING DATE: 2001-06-18
| PRIOR FILING DATE: 2001-06-18
| NUMBER OF SEQ ID NOS: 2070
| SEQ ID NO 820
| LENGTH: 329
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                       LISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVVRVF 317
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Publication No US20040115676A1
| GENERAL INFORMATION:
| APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
| APPLICANT: MGUYEN, Danniel B.; THORNYON, Michael,
| APPLICANT: MGUYEN, Danniel B.; THORNYON, Michael,
| APPLICANT: MGNDHI, Ameena R.; CHAWLA, Narinder K.
| APPLICANT: HAFALIA, Amena R.; CHAWLA, Narinder K.
| APPLICANT: HAFALIA, April J.A.; RAMKUMAR, Jayalaxmi,
| APPLICANT: UIN, Pel; TAMG, Y. Tom,
| APPLICANT: GRAUL, Richard C.; KAHN, Farrah A.;
| APPLICANT: GRAUL, Richard C.; KAHN, Farrah A.;
| APPLICANT: WALSH, Roderick T.; ISON, Craig H.;
| APPLICANT: WARREN, Bridget A.; YANG, Junming;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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US-10-292-798-820
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                                                                                                 RESULT 14
US-10-292-798-820
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Matches 179;
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APPLICANT: LEE, ERDESTINE A.; HARLAND, LEE

TITLE OF INVENTION: G-PROTEIN COUPLED RECEIPTORS
CURRENT APPLICATION NUMBER: US/10/467,252
CURRENT FILING DATE: 2003-08-06
PRICR APPLICATION NUMBER: US/20/467,322
PRICR APPLICATION NUMBER: US 60/267,322;
PRICR APPLICATION NUMBER: US 60/267,322;
PRICR APPLICATION NUMBER: US 60/271,215
PRICR FILING DATE: 2001-02-03
PRICR FILING DATE: 2001-02-03
PRICR FILING DATE: 2001-03-08
PRICR FILING DATE: 2001-03-03
PRICR FILING DATE: 2001-03-03
PRICR FILING DATE: 2001-03-03
PRICR PLICATION NUMBER: US 60/280,597
PRICR FILING DATE: 2001-03-23
PRICR PLICR DATE: 2001-03-30
PRICR PLICR DATE: 2001-03-30
PRICR FILING DATE: 2001-03-30
PRICR PLICR DATE: 2001-03-30
PRICR PLICR DATE: 2001-04-05
PRICR PLICR DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 96
SOFTWARE PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7475226CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: September 15, 2004, 21:39:13
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Matches 179; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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OM protein - protein search, using sw model

September 15, 2004, 21:33:43; Search time 13 Seconds (without alignments) 1317.775 Million cell updates/sec Run on:

US-10-081-775-2 1718 1 MSSTLGHNNESPHHTDVDPS......RKRVVRVFQSGQGMGIKASE 329 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | , ; ' | | O E O | o mod | 2 homo | homo | homo | | rattr | 4 homo | у рошо | homo | homo | omou s | homo | homo | рошо | homo | homo | homo | homod | | homo | l homo | homod | homod 4 | bomod 8 | omod s | homo | homod | 1 | | рошо / |
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| * | Query Match | - | 54 | 52 | 51 | 51 | | | 20 | 20 | 20 | 20 | 20 | 20 | 49 | 49 | 48 | 48 | 48 | 4 | 4 | 4 | | 45 | 45 | 45 | 45 | 4 | 4 | 4 | 4 | 43 | 42 | 4 |
| | Score | 1649 | 931.5 | 904 | 889.5 | 885.5 | 883.5 | 881.5 | 873 | 871 | 867.5 | 866.5 | 866 | 861 | 847.5 | 842 | 838.5 | 838 | 830.5 | 822 | 808 | 801 | 788.5 | 788 | 88/ | 787 | | 782.5 | | 761.5 | 755 | 744.5 | 730 | 725.5 |
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| 40.9 | 40.9 | 40.5 | 39.6 | 39.4 | 39.2 | 38.9 | 36.2 | 36.2 | 35.6 | 34.5 | 33.5 |
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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  PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
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--- FUNCTION: Putative odorant receptor.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SUBCELLULAR LOCATION: Location the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the 
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Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
"Genome-wide discovery and analysis of human seven transmembrane helix
"Genome-wide discovery and analysis of human seven transmembrane helix
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (PO
                                                                                                                                 Score 1649; DB 1;
Pred. No. 4.7e-123;
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10-0CT-2003 (Rel. 42, Last Bequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Olfactory receptor 52L1.
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Pfam; PF00001; 7tm_1; 1.
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larity 98.8%;
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 TDLALSSTIVPKMLAILWLHAGEISFGGCLAQMFCVHSIYALESSILLAMAFDRYVAICN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 PLRYATILIDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKLA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell C.M., Felsenfeld G., Groudine M., Hardison R.; "Comparative structural and functional analysis of the olfactory receptor genes flanking the human and mouse beta-globin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLCMLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 5 N-LINKED (GLCNAC. . .) (POTENTIAL)
318 AA; 35121 MW; 178968087D613CB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.8%; Score 889.5; DB 1; Length 318; 52.6%; Pred. No. 3.3e-63; live 51; Mismatches 92; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODPSN.
PROSITE: PS050287; G_PROTEIN_RECEP_F1 1; 1.
PROSITE: PS50262; G_PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).
-!- FUNCTION: Putative odorant receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew, HGNC:15212, OR52D1.

GO; GO:0016021; C:integral to membrane; NAS.

GO; GO:0004984; F:olfactory receptor activity; NAS.

GO; GO:0007608; P:olfaction; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (POTENTIAL).
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        Olfactory receptor 52D1 (HOR5'betal4).
                                                                                                                                               MEDLINE=20570519; PubMed=11121057;
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102
1123
1142
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1163
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3118
                                         Homo sapiens (Human).
                                                                                                                            SEQUENCE FROM N.A.
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                                                                                         NCBI_TaxID=9606;
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WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 KPVYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 EPMFYFLAILSTIDLALSATSVPRMLGIFWFDAHEINYGACVAOMFLIHAFTGMEAEVLL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 AMAFDRYVAICHPLRYATILTDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILH 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 TYCEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVIRLSSHEARSK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 ALGTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKT 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.6%; Score 904; DB 1; Length 311; 54.3%; Pred. No. 2.3e-64; ive 54; Mismatches 82; Indels
                                                                                                                                                              EMBL; AB065530; BAC05777.1; -.
Genew; HGNC:14799; OR52J3.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PROSITE; PS000237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Last sequence update)
Last annotation update)
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KQIRERVLYVF 308
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Q9H346;
16-OCT-2001
16-OCT-2001
15-MAR-2004
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                                                                                                                                                                                                                                        75 MLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAAMAFDRYV 134
                                                                                                                                                                                                                                                              67 MLSFTDLVMCSSTIPKALCIFWFHLKDIGFDECLVQMFFIHTFTGMESGVLMLMALDRYV 126
                                                                                                                                                                                                                                                                                                                                    VKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTCGSH 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 ICAIVESYTPAFFSFESHRFGEHIIPPSCHIIVANIXLLLPPTMNPIVVGVKTKQIRDCV 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
Tsutsumi S., Aburatani H., Asai K., Akiyama Y.,
"Genome-wide discovery and analysis of human seven transmembrane helix
"Genome-wide discovery and analysis of human seven transmembrane helix
                                                                                                                                                                                                                                                                                                                                                                                                              15 TDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLC
                                                                                                                                                                                       7 TDLIPASFILNGVPGLEDTQLWISFPFCSMYVVAMVGNCGLLYLIHYEDALHKPMYYFLA
                                                                                                                                                                                                                                                                                                                  135 AICHPLRYATILIDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTYCEHMAV
                                                                                                                               Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                               1;
                                   .) (POTENTIAL)
                                                                                         Length 321;
                                                                                                                               Indels
                                       2 N-LINKED (GLCNAC. . .) (PC 321 AA; 36005 MW; A68363F08E3BA65C CRC64;
                                                                                         ; Score 885.5; DB 1
; Pred. No. 6.9e-63;
51; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Olfactory receptor 52L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00001; 7tm 1; 1. PROSITE; PS00237; PROTEIN_RECEP_F1_1; 1.
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Genew; HGNC:14788; OR52L2.
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Pfam; PF00001; 7tm_1; 1.
                                                                                           52.6%;
                                                                                                                                   Matches 162; Conservative
321
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298
999
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                                     CARBOHYD
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-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SUBILARITY: Belongs to family 1 of G-protein coupled receptors.
-i- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                        311
                     191
                                                                                                                                    LISYTPALFSFTHRFGHH-VPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVVRVF 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
Isutsumi S., Aburatani H., Asai K., Akiyama Y.;
"Genome-wide discovery and analysis of human seven transmembrane helix
 CGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTCGSHVCVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Eutel
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB065813; BAC06032.1; -.
Genew; HGNC:15230; OR52N4.;
InterPro; IPR00021; GPCR_Rhodpsn.
PARM: PF00001; 7tm i, 1.
PRINTS; PR00237; GFCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS0262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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EXTRACELLULAR (POTENTIAL).
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EXTRACELULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
Olfactory receptor 52N4.
                                                                                                                                                                                                                                                                                                                                            321 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
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                                                                                                                                                                                                             318 QSGQ 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                            OYN4 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsutsumi
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OYN4_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKALGICGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LPSNITSTH-----PAVFLLVGIPGLEHLHAWISIPPCFAYTLALLGNCTLLFIIRADAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 LHTYCEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 LGHNMESPHHTDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPV
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                                                                                                                                        Genew; HGNC:1522; ORS2KI.

InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm 1; 1.

PROSITE; PS00023; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

ROSITE; PS50262; G ROTEIN RECEP F1 2; 1.

Multigene family; Olfaction. EXTRARGIATH DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93; Indels
                                                                                                                                                                                                                                                                                                      z (FUTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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8045963357FAB634 CRC64;
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (1
                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.3%; Score 881.5; DB 1
53.2%; Pred. No. 1.4e-62;
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AC Q0NH56.
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2004 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DF 01-0CT-2004 (Rel. 43, Last annotation update)
GN 0852N5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Mismatches
                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                           4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC
                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                  EMBL; AB065790; BAC06009.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35289 MW;
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KTKOIREYVLSLFO 310
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TRANSMEM
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DISULFID
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-!- DATABASE: NAME-Human Olfactory Receptor Data Exploratorium (HORDE);
WWW-"http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols
                                                                                                                                                                                                                                                                                                                                                                                                                                                       138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Sato T., Okouchi I., Arita M., Futami K., Matsumoto S., Suwa M., Sato T., Okouchi I., Arita M., Futami K., Aburatani H., Asai K., Akiyama Y.; "Genome-wide discovery and analysis of human seven transmembrane helix
                                                                                                                                                                                                                                                                                                                                                                                                          PLRYATILTDT11AH1GVAAVVRGSLLMLPCPFFIGRLNFCQSHV1LHTYCEHMAVVKLA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. .) (POTENTIAL) 742CD45420A25A4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                 51.4%; Score 883.5; DB 1; Length 304; 57.7%; Pred. No. 9.5e-63;
         G_PROTEIN_RECEP_F1_2; 1. receptor; Transmembrane; Glycoprotein; Olfaction.
                                                                                                                                                                                                                                                                                                                                                               77; Indels
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                                                        EXTRACELLULAR (POTENTIAL).
                                                                                              2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                       4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                                                                 CYTOPLASMIC (POTENTIAL)
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10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Olfactory receptor 52K1.
                                                                     (POTENTIAL).
                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                              46; Mismatches
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                                                                                                                                                                                      5 (POTENTIAL)
CYTOPLASMIC (
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                                                      rAUSITE; PS50262; GG-protein coupled ri
Multigene family; Ol
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                                                                                                                                                                                                                                                                                                    304 AA;
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QBNGK4;
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SAIIITYVPAFFTFFFAHRFGGHTIPPSLHIIVANLYLLLPPTLNPIVYGVKTKQIRKSVI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                 16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Olfactory receptor 51B2 (G-protein coupled receptor RAIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AF079864; AAD12761.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
PEfam, PF00001; 7rm 1, 1.
PRINTS; PR000237; GFCRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
G-protein roughed receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99131082; PubMed=9932290;
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                                                                                                                                                                                                                                                                                                    (Rel. 40, Created)
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Best Local Similarity 53.6
Matches 165; Conservative
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320
                                                                                                                              KFFQGDKGAG 324
                                                                              RVFQSGQGMG 324
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FUNCTION: Putative odorant receptor.
FUNCTION: Putative odorant receptor.
SUNCELLUIAR DOCATION: Integral membrane protein.
SIMPLARITY: Belongs to family 1 of G-protein coupled receptors.
DATABAGE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol8
                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
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                                                                                                                                                          Siwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S., Isutsumi S., Aburatani H., Asai K., Akiyama Y.; "Genome-wide discovery and analysis of human seven transmembrane helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 VDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFL-CM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 VTPPSFILNGIPGLERVHVWISLPLCTMYIIFLVGNLGLVYLIYYEESLHHPMYFFFGHA
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                                          Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:15231; ORSINS.
InterPro; IPR000276; GPCR_Rhodpsn.
PRIMITS; PR000237; GFCRRHODDPSN.
PROSITE; PS00237; GFROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.8%; Score 873; DB 1; Length 324; 53.2%; Pred. No. 6.8e-62;
                                        Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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52; Mismatches
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                 sapiens (Human)
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Les 165; Conserv
                                                                                                                                        SEQUENCE FROM N.A.
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Tsutsumi
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-! - FUNCTION: Putative odorant receptor.
-! - SUBCELLULAR LOCATION: Integral membrane protein.
-! - SUBCELLULAR LOCATION: Integral membrane protein.
-! - SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-! - DATABASE: NAME-Human Olfactory Receptor Data Exploratorium (HORDE);
WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&v
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                                                                                                                                                                                                                                                                                                                                                                                                                            64 FLAMLATTDVGLSTATIPKMLGIFWINLRGIIFEACLTQMFFIHNFTLMESAVLVAMAYD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 RYVAICHPLRYATILTDITITAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTYCEH 191
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                                                                                                                                                                                                                                                                                                                                                       12 PHHIDVDPSVPFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYL
                                                                                                                                                                                                                                                                                                                                                                                                        72 FLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAMAFD
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Suwa M., Sato I., Okouchi I., Arita M., Futami K., Matsumoto S.,
Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
"Genome-wide discovery and analysis of human seven transmembrane helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                  4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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BC5D7D13A52059BA CRC64;
                  3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                      96;
                                                                                                                                                                                                                                                                50.5%; Score 867.5; DB 1; 52.6%; Pred. No. 1.8e-61;
                                                                                                                                                                                                               (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                    51; Mismatches
                                                                                                                                                                                              BY SIMILARITY.
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Matches 164; Conservative
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-:- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-:- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                   139
                                                                                                  LRYATILTDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKLAC 199
                                                                                                                                                                   259
                                                                                                                                                                                                                                                            248
                                                                                                                                                                                                                                                                                     260 ISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVVRVFQS 319
                                                                                                                                                                                                                                                                                                        89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Suro T., Okouchi I., Arita M., Futami K., Matsumoto S., Suwa M., Sato T., Okouchi I., Asai K., Akiyama Y.; "Genome-wide discovery and analysis of human seven transmembrane helix
                             DLAASVSTVPKLLAIFWCGAGHISAACLAHMFFIHAFCMMESTVLLAMAFDRYVAICHP
                                                                                                                                                                                                                200 GDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTCGSHVCVIL
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PRINTS; PR00037; GPCRHODOPSN.

PROSITE; PS00237; GPCRHODOPSN.

PROSITE; PS50262; GPROTEIN RECEP_F1 1; FALSE_NEG.

G-protein coupled receptor; Transmembrane; Glycoprotein; DOMAIN

Multigene family; Olfaction. RXTPARCETITIEN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor genes.", Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).
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(Rel. 43, Last annotation update)
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InterPro; IPR000276; GPCR_Rhodpsn.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                               BMBL; AB065538; BAC05784.1; -. denew; HGNC:14853; OR52N1.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PROSITE; PS000237; G_PROTEIN RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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15-MAR-2004 (Rel. 43, Last annotation update)
Olfactory receptor 52K2.
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Best Local Similarity
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-i- FUNCTION: Putative ogorant receptor.
-i- SUBCELLUIAR LOCATION: Integral membrane protein.
-i- SUMILARITY: Belongs to family 1 of G-protein coupled receptors.
-i- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
-i- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
-i- MWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAM 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
"Genome-wide discovery and analysis of human seven transmembrane helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MESPHHIDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKP
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                                                                                                   fitted (JUL-2001) to the EMBL/GenBank/DDBJ databases FUNCTION: Putative odorant receptor.
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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; Pred. No. 2.3e-61;
49; Mismatches 98
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N-LINKED (GLC)
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InterPro; 1PR000276; GPCR_Rhodpsn.

PROSITE; PR00037; G_PROTEIN RECEP_F11; 1.

PROSITE; PS50263; G_PROTEIN_RECEP_F12; 1.

Receptor; Transmembrane. EXTREMELIZAR.

DOMAIN
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CYTOPLASMIC (
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52.4%;
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Best Local Similarity
FROM N.A.
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EMBL; AF311306; AAG40776.1; -.
EMBL; AF369708; AAK38728.1; -.
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10-OCT-2003 (Rel. 42, Created)
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-i- TISSUE SPECIFICITY: Exclusively expressed in the prostate.
-i- SIMILARITY: Belongs to family 1 of G-protein compled receptors.
-i- DATABASE: NAME-Human Olfactory Receptor Data Exploratorium (HORDE);
-WWW-"http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W. Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

A Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Stapleton M., Soares M.B., Peters G.J., Abramson R.D., Mullahy S.J.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Ala S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarane P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Alakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Garimwood J., Schmutz J., Myers R.M.,

R Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R "Generation and initial analysis of more than 15,000 full-length
                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
Olfactory receptor 51E2 (Prostate specific G-protein coupled receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and genetic characterization of an evolutionarily conserved human olfactory receptor that is differentially expressed across
                                                                                                                                                                                                                                                                                                                                                                                                       Xia C., Ma W., Liu M.;
"Identification of a prostate-specific G-protein coupled receptor
                                                                                                                                                                                           Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                    protein-coupled receptor, is overexpressed in prostate cancer.";
Cancer Res. 60:6568-6572(2000).
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=21002538; PubMed=11118034;

Xu L.L., Stackhouse B.G., Florence K., Zhang W., Shanmugam N.,
Sesterbenn I.A., Zou Z., Srikantan V., Augustus M., Roschke V.,
Carter K., McLeod D.G., Moul J.W., Soppet D., Srivastava S.;
"PSGR, a novel prostate-specific gene with homology to a G
                                                                                                                                                                                                                                                                                                                                                                                                                                      (PSGR) that interacts with G alpha subunit in yeast two hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21564169; PubMed=11707321;
Yuan T.T., Toy P., McClary J.A., Lin R.J., Miyamoto N.G.
Kretschmer P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                   320 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences.";
                                                                                STANDARD;
301 IRESILGVF 309
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                                                                               OXE2 HUMAN Q9H255;
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                                                     RESULT 13
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PROSITE; PS00237; GFCRHODOPSN.

PROSITE; PS00267; G-PROTEIN RECEP_F1_1; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.

EXTRACELLULAR (POTENTIAL). z (POTENTIAL). EXTRACELLULAR (POTENTIAL). 4 (POTENTIAL). EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) 03582CC2AAB6E2C6 CRC64; 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL). 1 (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). 6 (POTENTIAL). (POTENTIAL) EMBL; AY033942; AAK57550.1; -.
EMBL; BC020768; AAH20768.1; -.
GGnew; HGNC:15195; OK51E2.
GG; GO:0016021; C:integral to membrane; NAS.
GG; GO:0004984; F:olfactory receptor activity; NAS.
GG; GO:0007668; P:olfaction; NAS.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1. N-LINKED (GLCNAC. (POTENTIAL) 7 (POTENTIAL). CYTOPLASMIC (P BY SIMILARITY. 2 (POTENTIAL)

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-i- FUNCTION: Putative odorant receptor.
--- SUBCELDULAR LOCATION: Integral membrane protein.
--- SUBCELDULAR LOCATION: Integral membrane protein.
--- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
--- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);
WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 MYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFAIHSLSGMBSTVLLAM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                         BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                        49.3%; Score 847.5; DB 1; Length 317; 52.4%; Pred. No. 6.8e-60;
                                                                                                                                                                                                                                                                                                              94; Indels
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                  90 N-LINKED (GLCNAC. . .) (PC
35271 MW; 8C7293AA7FBCA95C CRC64;
                                        S (FOIENTIAL):
EXTRACELLULAR (POTENTIAL)
                                                                           7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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10-OCT-2003 (Rel. 42, Last sequence update)
10-MRA-2004 (Rel. 43, Last annotation update)
01factory receptor 52N2.
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                             (POTENTIAL)
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Matches 162; Conservative
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317 AA;
                                                                                                                                                                                                                                                                                         Similarity
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OBNGIO;
     DOMAIN
TRANSMEM
                                                   DOMAIN
TRANSMEM
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RA Alacshul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Alacshul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S.A., McWann D.M., McKerman K.J., Malek J.A., Glubsarane P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Glubs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubs R.A.,

RA Whiting M., Madan A., Young A.C., Shevorenko Y., Bueffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

C. -- SUBCELLULAR LOCATION: Integral membrane protein.

C. -- SUBCELLULAR LOCATION: Integral membrane protein.

C. -- SUBCELLULAR LOCATION: Integral membrane protein.

C. -- SUBLARITY: Belongs to family 1 of G-protein coupled receptors.

C. -- SUBLARITY: Belongs to family 1 of G-protein coupled receptors.

C. -- DATABASE: NAME=Human olfactory Receptor Data Exploratorium (HORDE):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                Buwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S., Futsumi S., Aburatani H., Asai K., Akiyama Y.; 'Genome-wide discovery and analysis of human seven transmembrane helix
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000276; GPCR_Rhodpen.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G_POTEIN_RECEP_F1_1; 1.
PROSITE; PS002407; TROUBLY RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
     10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Olfactory receptor 5181.
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MEDLINE=22388257; PubMed=12477932;
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188
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141 CYTOPLASMIC (POTENTIAL).
162 4 (POTENTIAL).
198 EXTRACELLULAR (POTENTIAL).
219 5 (POTENTIAL).
230 CYTOPLASMIC (POTENTIAL).
240 6 (POTENTIAL).
250 6 (POTENTIAL).
250 7 (POTENTIAL).
27 7 (POTENTIAL).
297 7 (POTENTIAL).
297 7 (POTENTIAL).
297 8 SIMILARITY.
297 1 (POTENTIAL).
297 8 SIMILARITY.
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329 8 SIMILARITY.
329 8 SIMILARITY.
35940 MW, A08A2658BD26477C CRC64;
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## Genew; HGNC:15228; OR52N2.
### Genew; HGNC:15228; OR52N2.
### Genew; HGNC:15228; OR52N2.
### IPR000201; Trm 1; 1.
### PFO0001; Trm 1; 1.
### PROSITE; PS00237; GPRCHODOPSN.
### PROSITE; PS00237; GPROTEIN RECEP_F1_2; 1.
### G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
### G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
### G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
### G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
### G-protein;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.0%; Score 842; DB 1; Length 321; 48.6%; Pred. No. 1.9e-59; Live 62; Mismatches 97; Indels
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Matches 156; Conservative
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Q8VG23
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| 911DA80 | 07trr5 | 08v£28 | 06nw60 | OBVGW | 08vh04 | Q7trr6 | 07tra8 | 08v£27 | Q7trr0 | Q8vgx4 | Q8vqy7 | 08vq24 | 08vgv | Q7trp9 | 07trs | 08v£06 | Q8vqw0 | 07trs0 | 09eda | QBvho3 | 6AqA8Ö | Q7trp3 | 08vq8 | 07trr7 | O8vew8 | OBVh00 | Ognak5 homo | Q8vgw5 |
| OBVGU9 | Q7TRR5 | QBVF28 | 06DM6Ö | Q8VGW2 | Q8VH04 | Q7TRR6 | Q7TRQ8 | Q8VF27 | Q7TRR0 | Q8VGX4 | Q8VGY7 | Q8VG24 | Q8VGV9 | Q7TRP9 | Q7TRS2 | Q8VF06 | Q8VGW0 | Q7TRS0 | Q9EQQ6 | Q8VH03 | Q8VBV9 | Q7TRP3 | Q8VG84 | Q7TRR7 | QSVEWS | Q8VH00 | OBNGK5 | Q8VGWS |
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| 317 | 316 | 327 | 339 | 312 | 317 | 312 | 316 | 341 | 314 | 312 | 317 | 316 | 319 | 324 | 314 | 312 | 319 | 314 | 314 | 316 | 320 | 312 | 308 | 314 | 314 | 318 | 317 | 322 |
| 51.4 | 51.4 | 51.4 | 51.4 | 51.4 | 51.3 | 51.3 | 51.1 | 51.0 | 50.9 | 50.8 | 50.8 | 50.7 | 50.7 | 50.7 | 50.6 | 50.6 | 50.6 | 50.5 | 50.4 | 50.3 | 50.3 | 50.3 | 50.1 | 49.9 | ο. | 49.6 | 49.6 | 49.5 |
| 883.5 | 883 | 883 | 883 | 882.5 | 881.5 | 880.5 | 877.5 | 877 | 875 | 873.5 | 873 | 871.5 | 871 | 871 | 870 | 868.5 | 868.5 | 867.5 | 998 | 865 | 865 | 864.5 | 860.5 | 858 | 854 | 852 | • | 851 |
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| utel. Murii ."; es. | | | Length 3 | els |
| e) Elae; Elae; Elae; Alae; Ala | | CRC64; | Len | Indels |
| T. 1 QBVGX9 PRELIMINARY; PRT; 329 AA. QBVGX9; QL-MAR-2002 (TrEMBLrel. 20, Created) O1-MAR-2002 (TrEMBLrel. 20, Last sequence update) O1-MAR-2002 (TrEMBLrel. 24, Last annotation update) O1-MAR-2002 (TrEMBLrel. 24, Last annotation update) O1-MAR-2002 (TrEMBLrel. 24, Last annotation update) O1-MAR-2002 (TrEMBLrel. 24, Last annotation update) O1-MAR-2002 (TrEMBLrel. 24, Last annotation update) O1-MAR-2002 (TrEMBLrel. 24, Last annotation update) O1-MAR-2003 (Condata; Craniata; Vertebrata; Eute Mammalai; Eutheria; Rodentia; Sciurognathi; Muridae; Muri NGEL TaxID=10090; L1 SEQUENCE FROM N.A. And X., Firestein S.J.; MAL Neurosci. 0:0-0(2002). [2] SEQUENCE FROM N.A. Adams M.; SUDMItted (JAN-2002) to the EMBL/GenBank/DDBJ databases. BMBL; AV073012; AAL60675 1; - GO; GO:0016021; Cintegral to membrane; IEA. GO; GO:0016021; Cintegral to membrane; IEA. GO; GO:00186; P:G-procein coupled receptor activity; IEA. GO; GO:000188; F:rhodopsin-like receptor activity; IEA. GO; GO:000186; P:G-procein coupled receptor protein significan; PPO:0001; 7tm_1; 1. | | | DB 11; | 21; |
| 329 AA. ence up tation i a; Verte nathi; h ily of t ilx of t EA. EA. | | 0861 | DB Re-1 | ່ |
| 329 uenco otat. Tai, gnat) gnatly nily lEA. lEA. | 2, 1 | 7D23203F650861EF | Score 1534; DB 11 Pred. No. 8.8e-135 | 18; Mismatches |
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| Created) Last sectors and the complete of the | N. RECEI | | Sco | 8; |
| 99 90 WOX99 PRELIMINARY; PRT; 329 AA. 98 WOX29; 101-MAR-2002 (TrEMBLrel. 20, Created) 101-MAR-2002 (TrEMBLrel. 20, Last sequence up 101-JUN-2003 (TrEMBLrel. 24, Last annotation 101-JUN-2003 (TrEMBLrel. 24, Last annotation 101-JUN-2003 (TrEMBLrel. 24, Last annotation 101-JUN-2003 (TrEMBLrel. 24, Last annotation 101-JUN-2003 (TrEMBLrel. 24, Last annotation 101-JUN-2003 (TrEMBLrel. 24, Last annotation 101-JUN-2003 (TrEMBLrel. 24, Last annotation 101-JUN-2003) 101-JUN-2002 (Tordata; Rodentia; Vert 101-JUN-2002) 101-JUN-2002 (TrEMBL/GenBank/DDB 102-MAGNER FROM N.A. 102-MAGNER FROM N.A. 103-MAGNER FROM N.A. 103-MAGNER FROM N.A. 104-MAGNER FROM N.A. 104-MAGNER FROM N.A. 105-MAGNER M.A. 105-MAGNER FROM N.A. 105-MAGNER FRO | PRINTS; PRO0237; GPCRRHODOPSN. PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; Receptor. | 36285 MW; | 89.3%; | |
| QUOKAS QUEST Q | PROT | 3628 | 889. | Conservative |
| T 1 9 90 (2002) 60 (2002) 10 - MAR-2002 (TrEMBLrel. 01 - MAR-2002 (TrEMBLrel. 01 - MAR-2003 (TrEMBLrel. 01 - MAR-2003 (TrEMBLrel. 01 - MAR-2003 (TrEMBLrel. 01 - MAR-2003 (TrEMBLrel. 01 - MAR-2003 (TrEMBLrel. 01 - MAR-2003 (TrEMBLrel. 01 - MAR-2003 (TrEMBLrel. Mammalia; Eutheria; Rod. NCBL TaxID=10090; [1] SEQUENCE FROM N.A. Adams N., Firestein S.J. Nat. Neurosci. 0:0-0(20) [2] SEQUENCE FROM N.A. Adams M.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. Adams M. (JAN-2002) to SEQUENCE FROM N.A. SEQUENCE FROM N.A. Adams M. (JAN-2002) to SEQUENCE FROM N.A. Adams M. (JAN-2002) to SEQUENCE FROM N.A. SEQUENCE FROM N.A. Adams M. (JAN-2002) to SEQUENCE FROM N.A. SEQUENCE FROM N.A. Adams M. (JAN-2002) to SEQUENCE FROM N.A. SAD (30:001684; F:receptor 30: GO:0001584; F:receptor | 9 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | Ą; | Ltv | serva |
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| 9 080GX9 080GX9; 01-MAR-20 01-MAR-20 01-MAR-20 01-MAR-20 01-GACO-20 01 | PRINTS; F PROSITE; PROSITE; Receptor. | SEQUENCE | Matc | s 2 |
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| RESULTA OR VGX9 OR | X | S O | B G | Ma |

1 MSSTLGHNMESPHHTDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVA 60

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121 AFDRYLAICRPLHYGSLLSSESVSKLGAAALLRGLGLMTPLTCLLARLSYC-GRVVAHSY 179
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.; IEA.
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Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
Walker M., Williams E.M., Axel R., Trask B.J.;
"Odorant receptor ESTs demonstrate olfactory expression of over 400
genes, extensive alternate splicing, and unequal expression levels.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN2013) to the EMBL/GenBank/DDBJ databases.

EMBL; AV17340; AAL61003.1; -.

EMBL; AV217664; AAP71043.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016872; F:receptor activity; IEA.

GO; GO:0001864; F:rhodopsin-like receptor activity; IEA.

GO; GO:000186; P:G-protein coupled receptor protein signalin. ..;

R GO; GO:0001786; P:G-protein coupled receptor protein signalin. ..;

R FRINTS; PRO0275; GPCR-Rhodpsn.

R PRINTS; PRO0237; GPCRR-DOPSN.

R PROSITE; PS00237; GPRCTEIN_RECEP_F1_1; 1.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01factory receptor MNR29-1 (Olfactory receptor GA x6K02T2BHJ9-5307445-5306498).
GA_X6K02T2BHJ9-5307445-5306498.
Bubaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Zhang X., Firestein S.J.;
"The Olfactory receptor gene superfamily of
"The Neurosci. 0:0-0(1202).
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Best Local Similarity 56.4<sup>3</sup>
Matches 176; Conservative
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241 QEARSKALGTCGSHVCVILISYTPALFSFFTHRFGHHVPLHIHILLANVYLLFPPALNPV
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
Walker M., Williams E.M., Axel R., Trask B.J.;
"Odorant receptor ESTS demonstrate olfactory expression of over 400
genes, extensive alternate splicing, and unequal expression levels.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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            TEPVLHKPVYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMM
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-6CT-2003 (TrEMBLrel. 25, Last an
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 VYGVKTREIRERVAKVFQWGQGTRLKISK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYGVKTKQIRKRVVRVFQSGQGMGIKASE 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 AA;
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Olfactory receptor GA_x6K02T2PBJ9-7810071-7809121.
GA_X6K02T2PBJ9-781007I-7809121.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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SEQUENCE
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                                                                          240 GTCGSHLGVILLFYTPGLFSFYTQRFGQHVPRHVHILLADLYLVVPPMLNPI1YGMKTKQ 299
         GICGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQ 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TSTVPKLLALFWAKDAEINFGACAAQMFFIHGFSAVESGILLAMAFDRYLAICWPLHYGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
"Genome-wide discovery and analysis of human seven transmembrane helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|: : :|||||||||||||||:|
121 LLSPESVGKLGAAAVLRGLGLATFLTCLLARLSYC-SRVVAHSYCEHMAVVKLACGGTQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLCMLSTIDLAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 ILTDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKLACGDIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVVRVFQSG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AB065856; BAC06074.1; ...
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:G-protein coupled receptor protein signalin. ..
PITERPRO; IPR000275; GPCR Rhodopsn.
PFAM; PF00001; 7tm 1; DFM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.5%; Score 936.5; DB 4; Length 299; 58.4%; Pred. No. 3.8e-79; live 48; Mismatches 74; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor genes.", Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 AA; 32514 MW; 5812D24DC8CD8F4A CRC64;
                                                                                                                                                                                                                                           QBNGF2,
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 24, Last annotation update)
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                       309 IRKRVVRVFQSG 320
                                                                                                                                                     300 İRDGALRLLKRG 311
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                                                                                                                                                                                                                                   PRELIMINARY;
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Local Best Loca Matches

SEQUENCE Query Match

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RESULT 5 Q7TRN7

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82 AASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAMAFDRYVAICHPLR 141
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Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
Walker M., Williams E.M., Axel R., Trask B.J.;

'Odorant receptor ESTs demonstrate olfactory expression of over 400
genes, extensive alternate splicing, and unequal expression levels.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 FFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLCMLSTIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKOIRKRVVRVF 31.7
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 54.5%; Score 936; DB 11; Length 3 Best Local Similarity 59.1%; Pred. No. 4.5e-79; Matches 175; Conservative 46; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Sanders K.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY317806; AAP71152.1; -.
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 AA; 34759 MW; 471D578C6F5D6B4B CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
04 X6K0212PBJ9-7206970-7207923)
05 X6K0212PBJ9-7206970-7207923,
Mus musculus (Mouse)
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53.1%;
56.8%;
                                                                          EMBL; AY317666; AAP71045.1;
                                                                                                                                                     Query Match
Best Local Similarity 56.8†
Matches 172; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                  319 AA;
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                    FROM N.A.
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  [2]
SEQUENCE B
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                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                       . .; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGIAKLACASIKPNTIYGLTVALSVTGMDVVLIATSYILILQAVLRLPSKDAQFRAFSTC
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"Odorant receptor ESTs demonstrate olfactory expression of over 400 genes, extensive alternae splicing, and unequal expression levels.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHHTDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RYVAICHPLRYATILTDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTYCEH
                                                                            genes, extensive alternate splicing, and unequal expression levels.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                            over 400
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 23, Last annotation update)
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                      Tonnes-Priddy L., Ross J.A.,
                                                                                                                                                                                                                           GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; F:G-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodopsn.
PFGm; PF00001; 7tm_1; 1.
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0
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                Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross
Walker M., Williams B.M., Axel R., Trask B.J.;
"Odorant receptor ESTs demonstrate olfactory expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                     317 AA; 35455 MW; 8388AE74D7B2CC1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.0%; Score 927; DB 11; 55.6%; Pred. No. 3.1e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 3.16
44; Mismatches
                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0237; GECRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 55.69
les 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVVRVF 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313
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SEQUENCE FROM N.A.
                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                    PRINTS;
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Matches
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Q7TRS6
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79 IDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAMAFDRYVAICH 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLRYATILIDTIIAHIGVAAVVRGSLIMLPCPFFIG-RINFCOSHVILHTYCEHMAVVKL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTÇGSHVCV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVVRVF 317
                                                                                                                                                                                                                                                                                                                                                                                     11 PSSFWLTGIPGLESLHWWLSIPFGSMYLVAVVGNITILAVVKTERSLHOPMYFFLCMLAV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 IDLVLSTSTMPKLLAIFWFGACSIGLDACLVQMFFVHCFATVESGIFLAMAFDRYVAICD
                                                                                                                                                                                                                                                                                                                          PSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLCMLST
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                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                       Length 319;
                                                                                                                                                                                       ; Score 912.5; DB 11; Length; Pred. No. 7.1e-77; 45; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monse.";
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY073768; AAL61431.1; -.
EMBL; AY317667; AAP71046.1; -.
Sanders K.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                            35259 MW; DB5D88EA93733128 CRC64;
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Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence updat
01-OCT-2003 (TrEMBLrel. 25, Last annotation upc
01-OCT-20ry receptor MR25-1 (Olfactory receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang X., Firestein S.J.;
"The olfactory receptor gene superfamily of Nat. Neurosci. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GA_x6K02T2PBJ9-5356887-5357840).
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MLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCWMESTVLLAMAFDRYV 134
             67 MLATIDLGLSTATIPKMLGIFWFSFRVILFGACLTQMFFIHNFTGMESAVLLAMAYDRYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000276; GPCR_Rhodpsn.
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EMBL; AY317704; AAP71072.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00001; 7tm
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                                                                                                                                            135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTK 307
                                                                                                                                                                                                                                                                                                                    9
                                                                     IEA.
                                                                                                                                                                                                                                                                                                VYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YCEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKA
                                                                                                                                                                                                                                                                         MESPHHTDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes, extensive alternate splicing, and unequal expression levels.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A., Walker M., Williams E.M., Axel R., Trask B.J., "Odorant receptor ESTs demonstrate olfactory expression of over 4
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000184; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IRF000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                            DB 11; Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 311;
                                                                                                                                                                                           Score 907.5; DB 11; Lv.,
Pred, No. 2.1e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sanders K.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX317709; AAP71076.1; -.
                                                                                                                                                                  317 AA; 34969 MW; 098189C67F91DB8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35111 MW; AF0317C0147D261C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-ACT-2003 (TrEMBLrel. 25, Last annotation update)
01-ACT-2003 (TrEMBLrel. 25, Last annotation update)
04_X6K02T2PBJ9-5335234-5936169.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.9%; Score 891.5; DB 1.
56.4%; Pred. No. 6.2e-75;
iive 46; Mismatches 85
                                                                                                                                                                                                                                           45; Mismatches
                                                                                                                                                                                                  52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QIRKRVVRVFQSG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QIRDRLLQILKTG 313
                                                                                                                                                                                                                       Local Similarity 55.9
les 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 56.4*
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 AA;
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SEQUENCE 1
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7TRR4
                                                                                                                                                                                                                                      Matches
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74

1;

15 TDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLC

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245
                    195 VKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTCGSH 254
                                                                                                                                               VCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVV 314
AICHPLRYATILTDTIIAHIGVAAVVRGSLIMLPCPFFIGRLNFCQSHVILHTYCEHMAV 194
                                                                                                                                                                            246 VCVILAFYTPALFSFWTHRFGRNVPRYIHILLANLYVVVPPMLNPVIYGVRTKOIYDRVK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .; IEA.
                                                                                                 Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A., Walker M., Williams E.M., Axel R., Trask B.J.;
"Odorant receptor ESTs demonstrate olfactory expression of over 400 genes, extensive alternate splicing, and unequal expression levels.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang X., Firestein S.J.; "The olfactory receptor gene superfamily of the mouse."; Nat. Neurosci. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanders K.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence upda:
01-07-2003 (TrEMBLrel. 25, Last annotation up:
01-07-2003 (TrEMBLrel. 25, Last annotation up:
01-07-2003 (TrEMBLrel. 26, Last annotation up:
01-07-2003 (TremBlack)
01-08-2003 (Offactory receptor
03-2003 (Offactory receptor
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128

62

Gaps

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Indels

242

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249 GTCGSHVCVILISYTPALFSFFTHRF-GHHVPVHIHILLANVYLLLPPALNPVVYGVKTK 307
                                                                                                                                                                                                                                                                                                                                                               243 STCTAHICAIVESYSPAFFSFFSHRFGGHTIPPSCHIIVANIYLLLPPTWAPVYGVKTK 302
                                                                                                                                                                                                                     129 AFDRYVALCHPLRYATILTDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTY
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
Walker M., Williams E.M., Axel R., Trask B.J.;
"Odorant receptor ESTs demonstrate olfactory expression of over 400
genes, extensive alternate splicing, and unequal expression levels.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                               63 MYYFLAMLSLIDLVMCSSTIPKTLCIFWFHLKEIGFDDCLVQMFFIHTFTGMESGVLMLM
                                                                                                                                                                                                                                                                                    189 CEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKAL
                                                                                           9 MESPHHTDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATBPVLHKP
                                                                                                                                                         69 VYLFICMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001586; F:G-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodopsin.
PF00001; 7tm_1; 1.
                                  DB 11; Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sanders K.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX072998; AAL60661.1; -.
EMBL; AX317684; AAP71059.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases
84FE6A4B4978C936 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
01factory receptor MOR30-1 (Olfactory receptor
0A x6K0212PBH9-559925-5598351).
0A x6K0212PBH9-559925-5598351.
Mus musculus (Mouse)
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   36060 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             303 QIRDCVIRILSGSK 316
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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      AA;
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                                                  Similarity
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      323
                                                                    Matches 165;
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      SEQUENCE
                                     Query Match
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                                                    Best Local
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                                                                                                                                                                132 RYVAICHPLRYATILTDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTYCEH 191
                                                                                                                                                                                                                                                                                        252 GSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLEPPALNPVVYGVKTKQIRK 311
                                                                                                                                  64 FLAMLATIDLGLSTATIPKMLGIFWINLREILFEDCLIQMFFIHKFTLMESTVLLAMAYD 123
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                                                         4 PNDTQFHPSTFLLIGIPGLESLHIMIGFPFCVVYMIALLGNLTLFVIKTESSLHQPMFY
                                                                                                   72 FLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAMAFD
                                                                                                                                                                                   MAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTC
                                                                                                                                                                                                                                              expression levels.";
                                       12 PHHIDVDPSVFFLLGIPGLEOFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYL
         Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodopsn.
PFam; PF00001; 7tm_1; 1.
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY073039; AAL60702.1; -.
EMBL; AX317779; AAP71131.1; -.
         Indels
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
         93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Olfactory receptor
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PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.
         49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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GA X6KO2T2PBJ9-7273558-7272587.

Mus musculus (Mouse).
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             Conservative
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             168;
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Q8VGV5
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Best Local Similarity 51.4
Matches 165; Conservative
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                                                                                                                                                Receptor.
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                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                              68
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"Odcant receptor ESTS demonstrate olfactory expression of over 400 genes, extensive alternate splicing, and unequal expression levels."; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                              9 MESPHHTDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKP
                                                                                                                                                                    Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                          Length 314;
                                                                                                                                                                    94; Indels
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY073252; AAL60915.1; -.
EMBL; AY317732, AAP71093.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                    314 AA; 35577 MW; 718EFEF2F351F669 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01factory receptor MOR31-10 (Olfactory receptor
GA_X6K02T2BBJ9-6306B19-6307775)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang X., Firestein S.J.;
"The olfactory receptor gene superfamily of the Nat. Neurosci. 0:0-0(2002).
                                                                                                                          51.8%; Score 890; DB 11; 53.9%; Pred. No. 8.7e-75;
                                                                                                                                                                    49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 AA
                    PROSITE, PS00237; G PROTEIN RECEP F1 1; 1. PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
PR00237; GPCRRHODOPSN
                                                                                                                                                                      Conservative
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Best Local Similarity
Matches 167; Conserv
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"Odorant receptor ESTs demonstrate olfactory expression of over 400
                                  ·:
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI TaxID=10090,
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR00102; GPCR.Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRAHODPSN.
PROSITE; PS00237; GPROTEIN RECEP FI 1; 1.
PROSITE; PS50262; GPROTEIN_RECEP_FI 2; 1.
                                                                                                                                                                                                                                                                                                                                  8;
                                                                                                                                                                                                                                                                              Length 318;
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                    318 AA; 35675 MW; A0B3CCE7A6A399F5 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01factory receptor MOR34-7 (Olfactory receptor
GA_X6K02T22BBJ9-7509539-7510489).
                                                                                                                                                                                                                                                                                                                                     86;
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                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                           51.8%; Score 890; DB 11; 51.4%; Pred. No. 8.8e-75;
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ive 62; Mismatches
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298 IYGVKTKQIQERVIQVFSLGK 318
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SEQUENCE
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Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
Walker M., Williams E.M., Axel R., Trask B.J.;
"dorant receptor ESTS demonstrate olfactory expression of over 400
genes, extensive alternate splicing, and unequal expression levels.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                      EMBL; AY317786; AAP71136.1; -0.00 co. 0.00 co. 0.0016021. Clintegral to membrane; IRA. GO; GO:0016021; Clintegral to membrane; IRA. GO; GO:0004872; F:receptor activity; IRA. GO; GO:0001584; F:rhodopsin-like receptor activity; IEA. GO; GO:0007186; P:G-protein coupled receptor protein signalin. InterPro; IPR000276; GPCR_Rhodopsn.
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                   51.7%; Score 887.5; DB 11; Length 316; 52.9%; Pred. No. 1.5e-74;
                                                                                                                                                                                                                                                                                                                                                                                     89; Indels
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                                                                                                                                                                                                                                                                                      316 AA; 35523 MW; 62424FB2A8260EB0 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01factory receptor MOR31-9 (01factory receptor
GA_X6K02T2PBJ9-6320148-6321104).
Mus musculus (Mousa)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae,
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"The olfactory receptor gene superfamily of the
Nat. Neurosci. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                     56; Mismatches
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                                                                                                                                                                              PRINT, 1. PRO0237; GPCRRODODEN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; GPROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                         Local Similarity 52.9
les 164; Conservative
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01-MAR-2002
                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                     EMBL; AY013041; AAB6704.1; ---
EMBL; AY013041; AAB6704.1; ---
EMBL; AY317733; AAP71094.1; --
GO; GO:001621; C:integral to membrane; IEA.
GO; GO:001884; F:receptor activity; IEA.
GO; GO:0001884; F:receptor activity; IEA.
GO; GO:0001884; F:receptor activity; IEA.
GO; GO:0001884; F:receptor activity; IEA.
FO: GO:0001884; F:receptor activity; IEA.
GO; GO:0001884; F:receptor activity; IEA.
FO: GO:0001884; F:receptor activity; IEA.
FO: GO:0001884; F:receptor activity; IEA.
FINITS: PRO0037; GPRRHDODEN.
FROSITE; PSE00237; GPRRHDODEN.
FROSITE; PSE00237; GPRRHDOPEN.
FROSITE; PSE00237; GPROTEIN RECEP_F1_1; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.7%; Score 887.5; DB 11; Length 318; 51.3%; Pred. No. 1.5e-74; ive 63; Mismatches 86; Indels 1;
                            Sanders K.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                       318 AA; 36248 MW; C8B74701E2CB1AEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 158; Conservative
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SEQUENCE FROM N.A.
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Search completed: September 15, 2004, 21:37:29
Job time : 46 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

September 15, 2004, 21:32:48; Search time 57 Seconds (without alignments) 1630.844 Million cell updates/sec : 0 Run

US-10-081-775-2 Perfect score: Title:

1 MSSTLGHNMESPHHTDVDPS.....RKRVVRVFQSGQGMGIKASE 329 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB s Maximum DB s

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

A_Geneseq_29Jan04:* Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Description | Abo42809 Human G-D | Aau24646 Human olf | Human | Human | Human GF | G-cont | | | Human | | 2 Human | O Human | - | Human | Aau10309 G-protein |
|-------------|---------------|--------------------|--------------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|--------------------|
| SOUTHWANTES | ΩI | ABO42809 | AAU24646 | ABP51578 | ABP51577 | ABP95772 | AAU85266 | ADC86345 | AAG71674 | AAU80511 | AAU95725 | ABR01673 | AAG71876 | ABR01670 | ADC86381 | AAG72396 | AAG71545 | AAB71366 | ABP95753 | AAU95700 | ADC86367 | AAE06752 | ABB44530 | AAG71562 | ABB44528 | AAU10309 |
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| | Length DB | 329 | 329 | 329 | 329 | 329 | 329 | 329 | 321 | 321 | 321 | 316 | 329 | 316 | 299 | 314 | 314 | 329 | 329 | 329 | 329 | 326 | 311 | 311 | 311 | 311 |
| * | Query | 100.0 | 98.4 | 98.4 | 98.4 | 98.4 | 98.4 | 98.4 | 96.0 | 96.0 | 96.0 | 80.1 | 9.95 | 55.3 | | 54.2 | 54.2 | 54.2 | 4 | 54.2 | 4 | 53.6 | N | 52.6 | 52.6 | 52.6 |
| | Score | 1718 | 1691 | 1691 | 1691 | 1691 | 1691 | 1691 | 1649 | 1649 | 1649 | 1376 | 972.5 | 950.5 | 936.5 | 31 | m | 931.5 | m | m | 931.5 | 920 | 907 | 904 | 904 | 904 |
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| Aau24572 Human olf Abp95702 Human GPC Aau35730 Human olf Aan85190 Ruman olf | | Abg76782 Human G-p Abg76869 Human G-p Aag72154 Human olf Aau24566 Human olf | Human Human G-coup G-prot | Abp51560 Human G p Aag72501 Human OR- Abp51561 Human G p Abo19498 Mouse GPC Aag72618 Murine OR |
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| AAU24572 ABP95702 AAU95730 | ADC86331 ABB44529 ABP51572 | ABG76782 ABG76869 AAG72154 AAU24566 | ABP95694 AAU95718 AAU85186 ABO42812 | ABP51560 AAG72501 ABP51561 ABO19498 AAG72618 |
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| 2 5 5 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 3930 | 2 4 2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 337 338 409 | 14444 1444 1443 |

ALIGNMENTS

RESULT 1

Human; G-protein coupled receptor; HGPRBMY25; immune disease; inflammatory disease; arthritis; asthma; AIDS; psoriasis; graft-versus-host disease; systemic lupus erythematosus; reproductive disorder; varicocele; orchitis; neural disorder; Alzheimer's disease; Parkinson's disease; depression; schizophrenia; cardiovascular disorder; hypertension; acute heart failure; pulmonary disorder; endocrine disorder; obesity; diabetes; anorexia; bone disorder; osteoptorsis; pain; cancer; chromosome identification; gene therapy; receptor. Human G-protein coupled receptor HGPRBMY25. ABO42809 standard; protein; 329 AA. (first entry) 22-SEP-2003 ABO42809; ABO42809 ID ABO4

US2003060409-A1. Homo sapiens.

27-MAR-2003.

21-FEB-2001; 2001US-0270134P. 27-MAR-2001; 2001US-0278952P. 21-FEB-2002; 2002US-00081775. (RAMA/) RAMANATHAN C S. (FEDE/) FEDER J N. (MINT/) MINTIER G A.

Mintier GA; Feder JN, Ramanathan CS,

WPI; 2003-521919/49. N-PSDB; ACD91434. New nucleic acid molecule encoding a human G-protein coupled receptor (HGPRBMY25) is useful for diagnosing, preventing or treating diseases involving the receptor, e.g. inflammation, diabetes, asthma, hypertension or cancer.

Claim 1; Fig 1A-B; 139pp; English.

The invention describes an isolated nucleic acid molecule comprising a

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sequence that is at least 95% identical to a polynucleotide encoding novel human G-protein coupled receptor HGFBMY25. The nucleic acid molecule, polypeptide and antibody are useful in diagnosing, preventing, treating or ameliorating medical conditions where GPCR is directly or indirectly involved, such as immune or inflammatory diseases (e.g. arthritis, asthma, AIDS, graft-versus-host disease, psoriasis or systemic lupus erythematosus), reproductive disorders (e.g. varicocele or orchitis), neural disorders (e.g. Alzheimer's disease, Parkinson's disease, depression or schizophrenia), cardiovascular disorders (e.g. hypertension or acute heart failure), pulmonary disorders (e.g. disease, endocrine disorders (e.g. obsenty, diabetes or anorexia), bone disorders (e.g. osteoporosis), pain or cancer. The polynucleotide may also be used in chromosome identification, in identifying organisms from minute biological samples, or as molecular weight markers. This is the amino acid sequence of a novel human HGPRBMY25 G-protein coupled receptor
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0; Mismatches 0;
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2000US-0192033P.
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2000US-0207702P.
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24-MAR-2000;
12-APR-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                     The invention relates to nucleic acids encoding human olfactory receptors, OR, (a g protein-coupled receptor, GPCR). The OR's specifically recognise molecules, odourants, that elicit specific olfactory sensation. The human olfactory receptors and polynucleotides encoding them are useful for screening a library of chemical compounds for compounds that are involved in olfactory sensation. Modulators of their activity are useful for pharmacological and genetic modulation olfactory signalling pathways. Therefore, they can be used in the food, pharmaceutical and cosmetic industries to customise odours and
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                                                                                                                                                                                                               Nucleic acids encoding human olfactory G protein-coupled receptors, useful for screening for compounds involved in olfactory sensation, the compounds can be used in the food, pharmaceutical and cosmetic
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Pred. No. 6.7e-178;
1; Mismatches 3;
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23-JUN-2000; 2000US-0213849P.
16-AUG-2000; 2000US-0226534P.
07-SEP-2000; 2000US-0230732P.
07-FEB-2001; 2001US-0266862P.
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Matches 325; Conservative
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2001US-0312902P CURAGEN CORP WPI; 2002-557660/59. N-PSDB; ABQ88372 Sequence 329 AA; 23-APR-2001; Homo sapiens 04-JAN-2001; 10-JAN-2001; 12-JAN-2001; 24-JAN-2001; 08-FEB-2001; 22-FEB-2001; 14-MAR-2001; 23-MAR-2001; 18-APR-2001; 16-AUG-2001; 27-JUN-2002 Gunther E, Li L, Pac Smithson (Zhong H, (CURA-)

immunomodulator; antiinflammatory; antidiabetic; anorectic; haemostatic; antibacterial; fungicide; protozoal; virucide; nephrotropic; osteopathic; cardiant; antiulcer; antiallergic; hepatotropic; antiparkinsonian; HUV; vaccine; gene therapy; cell signal processing; cardiomyopathy; diabetes; metabolic pathway modulation; atherosclerosis; cancer; obesity; asthma; allection; parkinson's disease; osteoporosis; Crohn's disease; ulcer; allergy; cirrhosis; glomerulonephritis; stroke; haematopoletic disorder; systemic lupus erythematosus. nootropic; anti-HIV; antiasthmatic; antiarteriosclerotic; cytostatic;

18-DEC-2001; 2001WO-US049347

2000US-0257876F 2001US-0259743P. 2001US-0260718P. 2001US-026148P. 2001US-0267464P. 2001US-0267464P. 2001US-0275946P. 2001US-0275946P. 2001US-0275946P. 2001US-0275946P. 2001US-0275946P.

Padigaru M, Ballinger RA, Kekuda R, Colman SD, Sciore P; on G, Peyman JA, Macdougall JR, Stone D, Vernet CAM, Shenoy S; c. , Millet I, Tchernev VT, Anderson D, Gusev V, Malyankar UM; 1, Ellerman KE, Wolenc A;

New isolated human G-protein coupled receptor X (GPCRX) polypeptide, useful for treating or preventing GPCRX-associated disorders e.g. diabetes, atherosclerosis, cancer or obesity.

Claim 1; Page 88; 354pp; English.

ABQBB154 to ABQBB417 represent human G protein coupled receptor (GPCR) C from the present invention. GPCR sequences can have neuroprotective, nootropic, anti-HIV, antiasthmatic, antiatreriosclerotic, cytostatic, moutopic, anti-HIV, antiasthmatic, antiatreriosclerotic, cytostatic, immunomodulator, antiinflammatory, antidiabetic, anorectic, haemostatic, antibacterial, fungicide, protozoal, virucide, nephrotropic, osteopathic, cardiant, antiuleer, and antialregic, hepatotropic and antiparkinsonian activities, and can be used in vaccines and gene therapy. GPCR proteins, nucleic acid molecules, and antibodies from the present invention can be used for manufacturing a medicament for treating or preventing a GPCR-casociated disorder or syndrome related to cell signal processing and metabolic pathway modulation, such as cardiomyogathy, atherosclerosis, diabetes, cancer, obesity, infections (bacterial, fungal, protezoal or viral), HIV, asthma, Parkinson's disease, osteoporosis, Crohn's disease, ulcers, allergies, cirrhosis, glomerulonephritis, stroke, systemic lupus erythematosus, or haematopoietic disorders. Anti-GPCR antibodies can be used diagnostically to monitor protein levels in tissues as part of a clinical testing procedure such as in determining the efficacy of a given treatment regimen. ABQB8418 to ABQB8639 represent PCR primers and probes for the human GPCRs of the present invention

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; G protein coupled receptor; GPCR; GPCRX; neuroprotective; incortopic; atti-HUV; antiathmatic; attiatrerioselerotic; cytostatic; immunomodulator; antialatematory; antidiabetic; anorectic; haemostatic; antibacterial; fungicide; protozoal; virucide; nephrotropic; osteopathic; cardiant; antiulacer; antiallergic; hepatotropic; antiparkinsonian; HIV; vaccine; gene therapy; cell signal processing; cardiomyopathy; diabetes; metabolic pathway modulation; atherosclerosis; cancer; obesity; asthma; infection; Parkinson's disease; osteoporosis; Crohn's disease; ulcer; systemic lupus erythematosus.
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                                           1 MSSTLGHNMESPHHTDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVA
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              Gaps
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              Indels
              3,
  Pred. No. 6.7e-178;
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              1; Mismatches
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21-DEC-2000; 2000US-0257876P.
04-JAN-2001; 2001US-0259743P.
12-JAN-2001; 2001US-0260718P.
12-JAN-2001; 2001US-0261498P.
24-JAN-2001; 2001US-0261699P.
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2001US-0271021P.
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98.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
              Conservative
  Best Local Similarity
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              Matches
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2001US-0275946P. 2001US-0278150P. 2001US-0284591P. 2001US-0285718P. 2001US-0299327P.

22-FEB-2001; 14-MAR-2001; 23-MAR-2001; 18-APR-2001; 23-APR-2001; 2001US-0312902P

19-JUN-2001

(CURA-) CURAGEN CORP

us-10-081-775-2.rag

06-MAR-2003

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ABQ88354 to ABQ88417 represent human G protein coupled receptor (GPCR) CDMA sequences, and ABP51560 to ABP51624 represent human GPCR proteins from the present invention. GPCR sequences can have neuroprotective, concropic, anti-HIV, antiasthmatic, antiatreriosclerotic, cytostatic, noctropic, antiah-HIV, antiasthmatic, antiatreriosclerotic, cytostatic, immunomodulator, antiahlammatory, antidiabetic, anorectic, haemostatic, antiabacterial, fungicide, protozoal, virucide, nephrotropic, osteopathic, cardiant, antiulcer, antiahlergic, hepatotropic and antiparkinsonian cullicated molecules, and antibodies from the present invention can be used in vaccines and gene therapy. GPCR proteins, nucleic acid molecules, and antibodies from the present invention can be used for manufacturing a medicament for treating or preventing a GPCR-casociated disorder or syndrome related to cell signal processing and metabolic pathway modulation, such as cardiomopathy, atherosclerosis, diabetes, cancer, obesity, infections (bacterial, fungal, protozoal or viral), HIV, asthma, Parkinson's disease, osteoporosis, Crohn's disease, ulcers, allergies, cirrhosis, glomerulomphritie, stroke, systemic lupus erythematosus, or haematopoletic disorders. Anti-GPCR antibodies can be clinical testing procedure such as in tissues as part of a clinical testing procedure such as in determining the efficacy of a given treatment regimen. ABQ88418 to ABQ88639 represent PCR primers and probes
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                  adigaru M, Ballinger RA, Kekuda R, Colman SD, Sciore P; G, Peyman JA, Macdougall JR, Stone D, Vernet CAM, Shenoy S; E, Millet I, Tchernev VT, Anderson D, Gusev V, Malyankar UM; Ellerman KE, Wolenc A;
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                                                                                                                                                                                               New isolated human G-protein coupled receptor X (GPCRX) polypeptide, useful for treating or preventing GPCRX-associated disorders e.g. diabetes, atherosclerosis, cancer or obesity.
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Pred. No. 6.7e-178;
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98.8%;
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                       Padigaru M,
                                                                                                                                WPI; 2002-557660/
N-PSDB; ABQ88371.
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                                                                 Gunther E,
                       Li L, Pac
Smithson (
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ABP95772 standard; protein; 329 AA

ABP95772;

ABP95772 ID ABPS XX AC ABPS

RESULT 5

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The invention relates to a method for screening G protein-coupled receptor (GPCR) genes (ABS42870-ABZ43216) and/or GPCR proteins (ABB95596-ABB95942) by extracting open-reading frames containing 6-8 transmembrane domains with 250-1000 amino acid residues to give a gene homologous with a known GPCR gene. The receptor proteins and encoded genes are useful for studying in vivo signal transduction mechanism and identifying targets for drug development e.g. based on olfactory and gustatory receptors in form of agonists and antagonists by screening intrinsic and extrinsic ligands as bitter taste inhibitors, taste enhances and fragrance improvers. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                            GPCR; G protein coupled receptor; signal transduction; olfactory;
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Pred. No. 6.7e-178;
1; Mismatches 3;
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                                                              Human GPCR polypeptide SEQ ID NO 354.
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13-FEB-2001; 2001JP-00034434.
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N-PSDB; ABZ43046.
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                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                 28-FEB-2002,
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The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the quanosine triphosphate-binding protein coupled receptor. The protein sequences shown in ADC85549-ADC8761 represent GPCR's of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ESTVLLAMAFDRXVAICHPLRYATILTDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TEPVIHKPVYLFLCMLSTIDILAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                           241 HEARSKALGTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPV
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SHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSS
                                                                HEARSKALGTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPCR; guanosine triphosphate-binding protein coupled receptor;
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                                                                                                                                                     301 VYGVKTKQIRKRVVRVFQSGQGMGIKASE 329
                                                                                                                                                                                  VYGVKTKQIRKRVVRVFQSGQGMGIKASE 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Human GPCR protein SEQ ID NO:798
                                                                                                                                                                                                                                                                                                        ADC86345 standard; protein; 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEPVLHKPVYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMM 120
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                                                                                                                                                                                                                                                                  odourant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Representing sensory perception of one or more odorants for the identification and design of tastes and odors comprises providing a representative group of n olfactory receptors.
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                                                                                                                                                                                                                                                                olfactory G-coupled receptor; sensory perception of composition; taste composition.
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Pred. No. 6.7e-178;
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                                                                                           AAU85266 standard; protein; 329 AA.
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                                                                                                                                                                                                                        G-coupled olfactory receptor #127
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13-MAR-2001; 2001US-00804291.
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N-PSDB; ABK37625.
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                                                                                                     HEARSKALGTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLLANVYLLLPPALNPV
                                                                                                                             241 HEARSKALGTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPV
                                 SHVILHTYCEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSS
                                                  Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encode polypeptides involved in olfactory olfactory agonists and antagonists.
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                                                                                                                                                                                                                                                                                                                                                                                                Human olfactory receptor polypeptide, SEQ ID NO: 1355.
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                                                                                                                                                                       VYGVKTKQIRKRVVRVFQSGQGMGIKASE 329
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(YEDA ) YEDA RES & DEV CO LTD
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24-FEB-2000; 2000US-0184809P.
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                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-inflammatory; anti-viral; gastrointestinal; cardiovascular; cerebroprocective; G-coupled receptor; cell proliferative disease; lymphoma; leukaemia; breast cancer; cirthosis; neurological disorder; stroke; Alzheimer's disease; multiple sclerosis; mental retardation; cardiovascular disease; multiple sclerosis; mental retardation; congestive heart failure; gastrointestinal disorder; dysphagia; AIDS; gastritis; autoimmune disorder; inflammatory disorder; Crohn's disease; systemic lupus erythematosus; metabolic disorder; diabetes; obesity; viral infection; herpesvirus; parvovirus;
61 VYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFIHAFCMMESTVLLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQ
                                                                                          VYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human G-coupled receptor (GCREC) protein, Seg ID No 19.
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Au-Young J;
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2000US-0208861P.
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07-JUN-2000; 2000US-0209868P
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Gandhi AR,
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N-PSDB; ABK16633.
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02-JUN-2000;
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Kallick DA,
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Claim 1; Page 133-134; 148pp; English

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Gaps

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Score 1649; DB 4; Pred. No. 2.8e-173; 1; Mismatches 3;

96.0%; 98.8%;

Matches 317; Conservative

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Similarity

Query Match Best Local (

Length 321; Indels 68

9 MESPHHIDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKP

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The invention relates to a novel human G-coupled receptor (I). (I) and its corresponding polynucleotides are useful for diagnosing, treating or preventing cell proliferative diseases (e.g. lymphoma, leukaemia, breast cancer or cirrhosis), neurological disorders (e.g. stroke, Alzheimer's disease, multiple sclerosis or mental retardation), cardiovascular diseases (e.g. atherosclerosis, angina pectoris or congestive heart failure), gastrointestinal disorders (e.g. dysphagia, indigestion or gastritis), autoimmune/inflammatory disorders (e.g. Apshagia, indigestion or systemic lupus erythematosus) or metabolic disorders (e.g. diabetes or obesity), or viral infections (e.g. infection by herpesvirus or parvovirus). Adu80493-AAU80515 represent novel human G-coupled receptor amino acid sequences of the invention
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Sequence 321 AA;

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                                                                            MESPNHIDVDPSVFFLLGIPGLEOPFLWLSLPVCGLGTATIVGNITILVVVATEPVLHKP
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Matches 317; Conservative
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Human olfactory and pheromone G protein-coupled receptor #212. AAU95725 standard, protein, 321 AA 02-JUL-2002 (first entry) AAU95725;

Human; olfactory and pheromone G protein coupled; receptor; GPCR;

tranquilizer, antidepressant, neuroleptic; endocrine, anabolic; anorectic; taste; fragrance; food additive; cosmetic; cell migration; sterility; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; depression; axonal growth; menstrual cycle; appetite sexual motivation; sexual attraction; aggression.

Homo sapiens

WO200224726-A2 28-MAR-2002 21-SEP-2001; 2001WO-BE000162

22-SEP-2000; 2000EP-00870211

The invention relates to olfactory and Pheromone G-protein coupled receptor (GPCR) or a protein 95% identical to the GPCR, a specific active portion and its encoding polymucleotide. Also included are an agonist, antagonist or inhibitor of the GPCR or the polymucleotide, a vector comprising the polymucleotide, a cell transformed by the vector, a non-human mammal comprising a partial or total deletion of the polymucleotide concoding the receptor and screening (detection and possibly, recovering) of compounds which are known or not known to be agonist, antagonists or inhibitors of natural compounds to the GPCR. The receptor-derived agonists, inhibitors or compounds are used as an improvement, elimination or substitution of an existing taste and/or a fragrance of (or in) the food and/or cosmetic products. They can also be used in the preparation of medicament in the treatment and/or prevention of a mammalian disorder, such as cell migration, sterility, psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, for promoting axonal growth, nerve cell connection and nerve regeneration for medulating male and female Novel pheromone G-protein coupled receptor and receptor-derived agonists, antagonists or inhibitors useful in food or cosmetic products or in the treatment or prevention of neurological disorders such as anxiety and Disclosure; Page 647-648; 833pp; English. 2002-330013/36 SA. N-PSDB; ABK68612 (CHEM-) CHEMCOM schizophrenia. Veithen A;

Gaps ; Length 321; 3; Indels Score 1649; DB 5; Pred. No. 2.8e-173; 1; Mismatches 3; 96.0%; Query Match Best Local Similarity 98.8 Matches 317; Conservative

Sequence 321 AA;

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behaviours, such as stimulation or suppression of appetite, sexual andivation, aggression and for promoting or suppressing chemical communication between organisms. The present sequence is a human olfactory and pheromone GPCR protein sequence prevention or the treatment by stimulation of several mammalian

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248 VYLELCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFIHAFCMMESTVLLAM 120 VYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAM 128 GTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQ 308 GTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQ 300 9 1 MESPNHIDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKP AFDRYVAICHPLRYATILTDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTY 121 AFDRYVALCHPLRYATILTDTIIAHIGVAAVVRGSLLMLPCPFLIGRLNFCQSHVILHTY CEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKAL 181 CEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKAL MESPHHTDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKP σ 69 129 189 249 241 61

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ABR01673 standard; protein; 316 AA ABR01673

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                                                                                                                      antiparkinsonian; nootropic; neuroprotective; tranquiliser; antirhemmatic; antiinflammatory; osteopathic; cardiant; neuroleptic; antiinflammatory; osteopathic; cardiant; neuroleptic; antiarthritic; gene therapy; olfactory g protein-coupled receptor; GPCR; infection; obesity; diabetes; hypertension; malnutrition; parkinson; disease; Albelmer's disease; Korsakoff's psychosis; anxiety; rheumatoid arthritis; chronic obstructive pulmonary disease; osteoporosis; asthma; myocardial infarction; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel human olfactory G protein-coupled receptors (GPCR) and their coding sequences (ABZ77872-ABZ77986 and ABR01571-ABR01685). The GPCRs and coding sequences are useful for diagnosing or treating a disease or condition associated with GPCR, e.g. infections, obesity, diabetes, hypertension, malnutrition, Parkinson's disease, Alzheimer's disease, Korreshoff, Es psychosis, anxiety, rheumatoid arthritis, chronic obstructive pulmonary disease, osteoporosis, asthma, myocaxdial infarction, schizophrenia, or osteoarthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 GDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVCVIL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New olfactory G protein-coupled receptor gene nucleic acid and polypeptide, useful for diagnosing or treating a disease or condition associated with GPCR, e.g. obesity, diabetes, hypertension, malnutrition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLAASVSTVPKILAI FWCGAGHISASACLAQMFFIHAFCMMESTVLLAMAFDRYVAICHP
                                                                                                      anorectic; antiasthmatic; antidiabetic; hypotensive; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLCMLSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEFILMGFPGIHTPLFFVFFLLLLFVSTIVGNITILVVVATEPVLHKPVYLFLCMLSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1376; DB 6
Pred. No. 4e-143;
                                                                      ID 206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
                                                                    G protein coupled receptor SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 102; 383pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sigurdsson GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.1%;
91.8%;
                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-2002; 2002WO-IB002481
                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-2001, 2001US-0301095P
                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2001; 2001US-0332758P
                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DECO-) DECODE GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-175284/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABZ77974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 316 AA;
                                                                                                                                                                                                                                                                                                                     WO2003000735-A2.
                                                                                                                                                                                                                                                 osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martinez RAM,
                                                                                                                                                                                                                                                                                  Homo sapiens.
                               17-APR-2003
                                                                                                                                                                                                                                                                                                                                                     03-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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                                                                      Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 VYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAM 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFDRYVAICHPLRYATILTDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 MESPHHIDVDPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                       Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yanai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glusman G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.7%; Pred. w.
tive 52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 1000-1001; 1857pp; English.
                                                                                                                                                                                Human olfactory receptor polypeptide,
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AAG71876 standard; protein; 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-OCT-2000; 2000WO-US027582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-1999; 99US-0158615P.
24-FEB-2000; 2000US-0184809P.
                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (YEDA ) YEDA RES & DEV
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DPSVFFLLGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLCMLS

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                                                                                                                                                                                                                                                                                                                                     Human; anorectic; antiasthmatic; antidiabetic; hypotensive; receptor; antiparkinsonian; nootropic; neuroprotective; tranquiliser; antirheumatic; antianflammatory; osteopathic; cardiant; neuroleptic; antiarthritic; gene therapy; olfactory G protein-coupled receptor; GPCR; infection; obesity; diabetes; hypertension; malnutrition; Parkinson's disease; Alzheimer's disease; Korsakoff's psychosis; anxiety; rheumatoid arthritis; chronic obstructive pulmonary disease; osteoporosis; asthma; myocardial infarction; schizophrenia;
                            239
                                                         308
                                                                                       299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel human olfactory G protein-coupled receptors (GPCR) and their coding sequences (ABZ77872-ABZ77866 and ABR015711-ABR01685). The GPCRs and coding sequences are useful for diagnosing or treating a disease or condition associated with GPCR, e.g. infections, obesity, diabetes, hypertension, malnutrition, Parkinson's disease, Alzheimer's disease, Korpaskoff's psychosis, anxiety, rheumatoid arthritis, chronic obstructive pulmonary disease, osteoporosis, asthma, myocardial infarction, schizophremia, or osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New olfactory G protein-coupled receptor gene nucleic acid and polypeptide, useful for diagnosing or treating a disease or condition associated with GPCR, e.g. obesity, diabetes, hypertension, malnutrition
              240 GTCGSHLGVILLFYTPGLFSFYTQRFGQHVPRHIHILLADLYLVVPPMLNPIIYGMKTKQ
CEHMAVVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKAL
                                                          GTCGSHVCVILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQ
                                                                                                                                                                                                                                                                                                                     Human G protein coupled receptor SEQ ID 200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 100-101; 383pp; English.
                                                                                                                                                                                                                            ABR01670 standard; protein; 316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUN-2002; 2002WO-IB002481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-2001; 2001US-0301095P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sigurdsson GT;
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                   IRKRVVRVFQSG 320
                                                                                                                                                  İWDGALRLLKWG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DECO-) DECODE GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2003-175284/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABZ77971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003000735-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martinez RAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                       17-APR-2003
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                                                                                                                     309
                              180
                                                         249
                                                                                                                                                   300
                                                                                                                                                                                                                                                          ABR01670;
189
                                                                                                                                                                                              RESULT 13
ABR01670
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The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The protein sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
                                              137
                                                                   197
                                                                                                                                              187
                                                                                                                                                                               257
                                                                                                                                                                                                              247
                                                                                                                                                                                                                                                                248 ILLFYTPGLFSFYTQRFGQHVPRHIHILLADLYLVVPPMLNPIIYGMKTKQIWDGALRLL 307
                                                                                                                                                                                                                                              258 ILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVVRVF 317
            68
129 WPLHYGSLLSPESVGKLGAAAVLRGLGLMTPLTCLLARLSYC-SRVVAHSYCEHMAVVKL
                                                                                                                                                                                                TIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAMAFDRYVAIC
                                                                                                                                                                               ACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTCGSHVCV
                                                                                                             138 HPLRYATILIDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              guanosine triphosphate-binding protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asai K, Akiyama Y, Aburatani H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; SEQ ID NO 834; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC86381 standard; protein; 299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human GPCR protein SEQ ID NO:834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUN-2002; 2002EP-00013517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUN-2001; 2001JP-00246789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-315783/31.
N-PSDB; ADC86380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 299 AA;
                                                                                                                                                                                                                                                                                                                                             K 308
                                                                                                                                                                                                                                                                                                                318 Q 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; GPCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JAN-2003.
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                                                78
                                                                                                                                                                                198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC86381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suwa M,
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
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Length 299;

DB 7;

54.5%; Score 936.5;

Query Match

ij

Gaps

ij.

Length 316; Indels

55.3%; Score 950.5; DB 6; 58.1%; Pred. No. 4.1e-96; tive 50; Mismatches 75;

Query Match 55.3 Best Local Similarity 58.1 Matches 175; Conservative

Sequence 316 AA;

nseq

Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be for determining differences in the olfactory faculties of different

individuals Sequence 314 AA;

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us-10-081-775-2.rag

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The present sequence is a polypeptide encoded by one of 344 newly mined human genes. It was used as a query sequence in a database search of olfactory receptor (OR)-like sequences. The invention relates to isolated polymucleotides encoding polypeptides involved in olfactory sensation. The polymucleotides can be used in screening for olfactory sensation. The polymucleotides allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents.
                                                                                                                   VSTVPKLLAIFWCGAGHISASACLAHMFFIHAFCMMESTVLLAMAFDRYVAICHPLRYAT 144
                                                                                                                                                         120
                                                                                                                                                                                          204
                                                                                                                                                                                                                                                           264
                                                                                                                                                                                                                                                                                           239
                                                                                       9
                                                  LGIPGLEQFHLWLSLPVCGLGTATIVGNITILVVVATEPVLHKPVYLFLCMLSTIDLAAS 84
                                                                       61 ISTVPKLLALFWAKDAEINFGACAAQMFFIHGFSAVESGILLAMAFDRYLAICWPLHYGS
                                                                                                                                                                                     145 ILTDTIIAHIGVAAVVRGSLLMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKLACGDTRP
                                                                                                                                                                                                       NRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTCGSHVCVILISYTP
                                                                                                                                                                                                                                                                                                                                        240 GLFSFYTQRFGQHVPRHIHILLADLYLVVPPMLNPIIYGMKTKQIMDGALRLLKWG 295
                                                                                                                                                                                                                                                                                                                       265 ALFSFFTHRFGHHVPVHIHILLANVYLLLPPALNPVVYGVKTKQIRKRVVRVFQSG 320
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotides which encode polypeptides involved in olfactory sation for identifying olfactory agonists and antagonists.
                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human OR-like polypeptide query sequence, SEQ ID NO: 2077.
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fuchs T,
   58.4%; Pred. No. 1.3e-94;
live 48; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glusman G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Page 1393; 1857pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG72396 standard; protein; 314 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lancet D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DIGI-) DIGISCENTS.
(YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-OCT-2000; 2000WO-US027582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1999; 99US-0158615P.
24-FEB-2000; 2000US-0184809P.
Best Local Similarity 58.4%
Matches 173, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sensation for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith D,
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